

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 00:00:13 ; Search time 3539 Seconds

(without alignments)
10819.839 Million cell updates/sec

Title: US-09-308-829-1

Perfect score: 936
Sequence: 1 caacctgactatctaattg.....gagcttacctctaattta 936

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_ov: *
5: gb_pat: *
6: gb_ph: *
7: gb_pl: *
8: gb_dr: *
9: gb_ro: *
10: gb_sts: *
11: gb_sy: *
12: gb_un: *
13: gb_vi: *
14: gb_ba: *
15: em_fun: *
16: em_hum: *
17: em_in: *
18: em_mu: *
19: em_om: *
20: em_or: *
21: em_ov: *
22: em_ph: *
23: em_pl: *
24: em_ro: *
25: em_sts: *
26: em_un: *
27: em_vi: *
28: em_ba: *
29: em_fun: *
30: em_hum: *
31: em_in: *
32: em_mu: *
33: em_om: *
34: em_or: *
35: em_ov: *
36: em_ph: *
37: em_pl: *
38: em_ro: *
39: em_sts: *
40: em_un: *
41: em_vi: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	936	100.0	936	1	STRSPEC	M35514 S.pyogenes
2	915.2	97.8	11277	1	AE010008	AE010008 Streptoco
3	910.4	97.3	10029	1	AE006523	AE006523 Streptoco
4	681.2	72.8	702	1	STREPEXCA	M97116 Streptoco
5	678	72.4	702	1	STREPEXCA	M97116 Streptoco
6	602.2	64.3	619	1	SPU02559	U02559 Streptoco
7	602.2	64.3	619	1	SPU02560	U02560 Streptoco
8	462.2	49.4	467	1	AF055699	AF055699 Streptoco
9	462.2	49.4	467	1	AF055700	AF055700 Streptoco
10	462.2	49.4	467	1	AF055701	AF055701 Streptoco
11	200.4	21.4	699	1	AF321000	AF321000 Streptoco
12	200.4	21.4	699	1	AF385523	AF385523 Streptoco
13	200.4	21.4	10107	1	AE006504	AE006504 Streptoco
14	148.6	15.9	50631	1	AE014139	AE014139 Streptoco
15	148.6	15.9	311600	1	AP005141	AP005141 Streptoco
16	148.4	15.9	10221	1	AE010021	AE010021 Streptoco
17	147	15.7	10947	1	AE006489	AE006489 Streptoco
18	139.8	14.9	633	1	AF233454	AF233454 Streptoco
19	139.8	14.9	705	1	AF124499	AF124499 Streptoco
20	139.6	14.9	10221	1	AE006536	AE006536 Streptoco
21	138.2	14.8	633	1	AF233455	AF233455 Streptoco
22	136.4	14.6	10439	1	AE009969	AE009969 Streptoco
23	135.4	14.5	633	1	AE233456	AE233456 Streptoco
24	127	13.6	50092	1	AE014148	AE014148 Streptoco
25	127	13.6	325650	1	AP005145	AP005145 Streptoco
26	123.8	13.2	3930	1	SDY489606	AJ489606 Streptoco
27	122.6	13.1	712	1	SDY294849	AJ294849 Streptoco
28	104.6	11.2	50354	1	AE014169	AE014169 Streptoco
29	104.6	11.2	323825	1	AP005146	AP005146 Streptoco
30	98	10.5	630	1	AF143659	AF143659 Streptoco
31	98	10.5	630	1	AF143670	AF143670 Streptoco
32	96.2	10.3	12601	1	AE006622	AE006622 Streptoco
33	94.8	10.1	630	1	AF143674	AF143674 Streptoco
34	94.6	10.1	10618	1	AE010110	AE010110 Streptoco
35	93.8	10.0	145265	2	AL935272	AL935272 Danio rer
36	93.2	10.0	630	1	AF086626	AF086626 Streptoco
37	93.2	10.0	630	1	AF143655	AF143655 Streptoco
38	93.2	10.0	630	1	AF143660	AF143660 Streptoco
39	93.2	10.0	630	1	AF143668	AF143668 Streptoco
40	92.6	9.9	155204	2	AC007926	AC007926 Trypanoso
41	91.6	9.8	630	1	AF143658	AF143658 Streptoco
42	91.6	9.8	630	1	AF143667	AF143667 Streptoco
43	91.6	9.8	771	1	SPY245405	AJ245405 Streptoco
44	91.6	9.7	629	1	AF143669	AF143669 Streptoco
45	90	9.6	630	1	AF143654	AF143654 Streptoco

ALIGNMENTS

RESULT 1
STRSPEC
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

STRSPEC 936 bp DNA linear BCT 26-APR-1993
S.pyogenes streptococcal pyrogenic exotoxin type C (spec) gene.
complete cds.
M35514
M35514.1 GI:153820
pyrogenic exotoxin.
Streptococcus pyogenes
Streptococcus pyogenes
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
1 (bases 1 to 936)
Goshorn,S.C. and Schlievert,P.M.
Nucleotide sequence of streptococcal pyrogenic exotoxin type C

Pred. No. is the number of results predicted by chance to have a

JOURNAL Infect. Immun. 56 (9), 2518-2520 (1988)
 MEDLINE 88314303
 PUBMED 3045005
 COMMENT Original source text: S.pyogenes DNA.
 FEATURES Location/Qualifiers
 source 1..936
 /organism="Streptococcus pyogenes"
 /mol_type="genomic DNA"
 /db_xref="taxon:1314"
 154..861
 /note="Streptococcal pyrogenic exotoxin type C (spec) precursor"
 /codon_start=1
 /transl_table=11
 /protein_id="AA027017.1"
 /db_xref="GI:153821"
 CDS 154..234
 /note="Streptococcal pyrogenic exotoxin type C signal peptide (put.); putative"
 235..858
 /product="streptococcal pyrogenic exotoxin type C"
 mat_peptide 144 c 127 g 301 t
 BASE COUNT 364 a 144 c 127 g 301 t
 ORIGIN
 Query Match 100.0%; Score 936; DB 1; Length 936;
 Best Local Similarity 100.0%; Pied. No. 1.3e-142;
 Matches 936; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CAACCTGACATTTAATGGAAGTGCACCTCTAAAGCAATATAATATACATTAT 60
 1 CAACCTGACATTTAATGGAAGTGCACCTCTCTAAAGCAATATAATATACATTAT 60
 61 AAAATTTCTAAATTAACAGAAATCTGATTTTAACTACTGCTATTTCTATTTCT 120
 61 AAAATTTCTAAATTAACAGAAATCTGATTTTAACTACTGCTATTTCTATTTCT 120
 121 CGTACGATTAATCATTTAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 121 CGTACGATTAATCATTTAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 121 CGTACGATTAATCATTTAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 181 GTTTTCATTAATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
 181 GTTTTCATTAATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
 181 GTTTTCATTAATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
 241 AAGAAGACATTTTGAATGTTAAAGTATTTTAACTACTGCTATTTCTATTTCTAT 300
 241 AAGAAGACATTTTGAATGTTAAAGTATTTTAACTACTGCTATTTCTATTTCTAT 300
 241 AAGAAGACATTTTGAATGTTAAAGTATTTTAACTACTGCTATTTCTATTTCTAT 300
 301 GATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
 301 GATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
 301 GATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
 361 AAATATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 361 AAATATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 361 AAATATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 421 TTTAAAGAGATGATCATGTAGATGTTTGAATTTAATTAATTAATTAATTAATTA 480
 421 TTTAAAGAGATGATCATGTAGATGTTTGAATTTAATTAATTAATTAATTAATTA 480
 421 TTTAAAGAGATGATCATGTAGATGTTTGAATTTAATTAATTAATTAATTAATTA 480
 481 GGTGAGTACATCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 481 GGTGAGTACATCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 481 GGTGAGTACATCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 541 TTGGGAATCTATTTATTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 541 TTGGGAATCTATTTATTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600

QY 601 GAAAGAGATATCGTAACCTTCCAGAAATGACTTTTAAATACAGAAATACCTATGAT 660
 DB 601 GAAAGAGATATCGTAACCTTCCAGAAATGACTTTTAAATACAGAAATACCTATGAT 660
 QY 661 AATTAATAAATTTATGACGCTACTTCTCTTATGTAAGCGGAGCAATGCAATGGCACA 720
 DB 661 AATTAATAAATTTATGACGCTACTTCTCTTATGTAAGCGGAGCAATGCAATGGCACA 720
 QY 721 AAGATGGAAGACATGAGCAATATGACTTATTTGACTCACCACCAATGAAGGACTAGTCA 780
 DB 721 AAGATGGAAGACATGAGCAATATGACTTATTTGACTCACCACCAATGAAGGACTAGTCA 780
 QY 781 GATATTTTTCGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
 DB 781 GATATTTTTCGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
 QY 841 GATATTTTATCTTGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
 DB 841 GATATTTTATCTTGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
 QY 901 GTTTTGTCTATCTCGAGGCTTACCTCTTAATTTTA 936
 DB 901 GTTTTGTCTATCTCGAGGCTTACCTCTTAATTTTA 936
 RESULT 2
 AE010008/c 11277 bp DNA linear BCT 03-APR-2002
 LOCUS
 DEFINITION Streptococcus pyogenes strain MGAS8232, section 56 of 173 of the complete genome.
 ACCESSION AE010008 AE009949
 VERSION AE010008.1 GI:19747945
 KEYWORDS
 SOURCE Streptococcus pyogenes MGAS8232
 ORGANISM Streptococcus pyogenes MGAS8232
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
 REFERENCE 1 (bases 1 to 11277)
 Smoot,J.C., Barblian,K.D., Van Gompel,J.J., Smoot,L.M., Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M., Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M., Zhang,Q., Kapur,V., Daly,J.A., Yeasly,L.G. and Musser,J.M. Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks
 Proc. Natl. Acad. Sci. U.S.A. 99 (7), 4668-4673 (2002)
 JOURNAL MEDLINE 21927593
 PUBMED 11917108
 REFERENCE 2 (bases 1 to 11277)
 Smoot,J.C., Barblian,K.D., Van Gompel,J.J., Smoot,L.M., Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M., Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M., Zhang,Q., Kapur,V., Daly,J.A., Yeasly,L.G. and Musser,J.M. Direct Submission
 Submitted (31-JAN-2002) Laboratory of Human Bacterial Pathogenesis/Rocky Mountain Laboratories/NIH/NIH, 903 S. 4th St., Hamilton, MT 59840, USA
 TITLE
 JOURNAL
 FEATURES
 source 1..11277
 /organism="Streptococcus pyogenes MGAS8232"
 /mol_type="genomic DNA"
 /strain="MGAS8232"
 /db_xref="taxon:186103"
 <1..9800
 misc_feature
 /note="phi spec"
 26..2002
 /gene="spyM18_0769"
 26..2002
 /gene="spyM18_0769"
 /note="best blastp match gblAAK33656.1 (AE006522) hypothetical protein, phage associated [Streptococcus pyogenes M1 GAS]"
 /codon_start=1

```
/transl_table=11
/product="hypothetical phage protein"
/protein_id="AAL97437.1"
/db_xref="GI:19747946"
/translation="MKIKSDAGRRTRKQFEIRKVLNRSKDIETIFARHISMTOTDIA
LKFVNGASVGALEIKENLVGDDTVKSDILTLGSEFNEIDKIGARALGV
AGSILVYGGVEFENRRTIILRKQGRKAPTVAGRNIVSEERLILGNYSIPY
VRYTPQKPEEAPGPHVGEKQPEPEQLTLEPILDGQYLSLVAQRRIOMVLSH
FNDKMKKEPTIEIRKLOKYLKDNVAGKYSIEVDYIDLSOTLDYODFRMEVE
LCOIPLVYKPKGITEESEKVEIYVDVYDSNHTIKIGTIGOSISKSLTGVSERIN
AENNOKVITNNKQFEINLPKILNDINGRWYKRPDDNIEHKIGDYEPKQKQKQK
TWIWDGHWKVLDTEDLNQRAFDPAEAMAEIKAKAQDEINQRTDKEEERAILK
NALPEBAIKKITEAIKVDIPISIKQSFDDLKNKVSSETSRINAEIILGNKTRYN
KNLVGDPNRTKTYDEDEYIEVANDGSGFRGTYTISQTCELLOKVAITLLOANK
GVLTLPPTAKTDQOTFEVTKDQOSIEVYPLSYTGVLGCDWKKPKQIDNASDTQEL
ALEMAKKEVYDGKDAITGIMSDSPQIILIDGCK"
1999..3009
/gene="hyLP"
/feature="synonym: spym18_0770"
1999..3009
/gene="hyLP"
/feature="best blastp match gb|AAK33900.1| (AE006545)
hyaluronidase - phage associated [Streptococcus pyogenes
M1 GAS]"
/codon_start=1
/transl_table=11
/product="hyaluronidase - phage associated"
/protein_id="AAL97438.1"
/db_xref="GI:19747947"
/translation="MTETIPLRVQFKRMATAEYTRSDVILLESIGFETPDGYAKFGD
KQOQFKRLKLNKPDIGAFQAKKETNSKITKLESSADKNAVYLKAEKLEIDKPLNT
KGGVMTGOLDFPKNGSGIKPSSVGCAINIDMKSEAGVYVYNNDSPTKMSLMT
GKETFNOSALFVYSGKTNAVNIAIROPTPNPSSALNITSGNENGSAQIRQVEAL
GRTKITHEPNENYANDENAAALSIDIVKKQKQKGAACGIYINSSTGTCGLLRK
NLCDDKFFYKHGSGFYAKKTSQIDGNLKNPADDHATKATVDSVKKALMLDK
QV"
3022..4908
/gene="spym18_0771"
3022..4908
/gene="spym18_0771"
/feature="best blastp match gb|AAK33658.1| (AE006522)
hypothetical protein, phage associated [Streptococcus
pyogenes M1 GAS]"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAL97439.1"
/db_xref="GI:19747948"
/translation="MSRDPPLTLDESNLYIGKDRVHYPTAEDNPKVYLASKCIQT
AHNQLMIERGQDATSYVAVVEGTGNPTGLFKDLKEISLETITANSQIMSKIKLT
NRGMLQDEYDGKIKTEIVNARGVATRISDGTDKLALINDTIDGIRREYRQDRRLS
SSYQINGIKQALQNDKIGLOAEIQTQGLSOKYDNEIRLSAKKITTTSSGTTTXY
ESKLACIRAEFTSNQGRRIEESQISGLRAVOQSTTSQISOETRDRTGAVSRVQDL
ESTQRLQDAEDNYSLLTHTVRGLQSDVGSPTGKIQSRLTQLAGQLEQRTVRGVMSI
ISAGDSIKLAIQKAGINAKMGSNETISAINNSYGVYTAGKHIALDGTNTNGFTT
TKTAEAKIRIADQIAGTIDARIIVINLASSIVGLDANFKIKAGIAGATYTLDEGV
IKRANGAMLIDISSAKMDENSNATINENSDNALVRRDTHTFVHFHSNAPKPYGGS
ALVASIGITSSSGVNSASGSRPAGRCFRHATGYNHTAIVDQTEITYQDSVLTADDES
INGEKFRRPKMKTKVLDMDLVYAAYVALGCMKHLANVGNTVHGNTNATVTELNH
INKI"
complement(4895..5419)
/gene="spym18_0773"
complement(4895..5419)
/gene="spym18_0773"
/feature="best blastp match hypothetical"
/feature="best blastp match hypothetical"
/codon_start=1
/transl_table=11
/product="hypothetical phage protein"
/protein_id="AAL97440.1"
/db_xref="GI:19747949"
/translation="MCACDSCAVKLMWFSCHPPIHSGVSPILLSNCSKMLSTRMISD
DVSSSHSKFKRSINRLEYSPLLTITSSASSLSSSSSLASASAMPLCSSMT
NSSLIAAVYISIKSVSFAYSLITLSTLASSIARPLARIIVILILISSTRYVLSLT
```

```
FFNVKSIVSPIKFC"
5351..5968
/gene="spym18_0774"
5351..5968
/gene="spym18_0774"
/feature="best blastp match gb|AAK33660.1| (AE006522)
hypothetical protein, phage associated [Streptococcus
pyogenes M1 GAS]"
/codon_start=1
/transl_table=11
/product="hypothetical phage protein"
/protein_id="AAL97441.1"
/db_xref="GI:19747950"
/translation="MRMKVYTGKYPQDSTGAVAATHIITAEAGSVISQVKKODLIS
TNTEFIKATLEEFKSEVEYIEAMGAOVQVDLEKISQETAKTAKTAQTAAGIARVS
AERTQKINLQTIHMLMSGKIDSIDIKGLLEIIEPAKKGEYQAYIVFYVDSKRED
GEAGEGNLVFVHNEAFEDKQTLLELESEAKVTAYKADVADQ"
5978..6253
/gene="spym18_0775"
5978..6253
/gene="spym18_0775"
/feature="best blastp match gb|AAK33661.1| (AE006522)
hypothetical protein, phage associated [Streptococcus
pyogenes M1 GAS]"
/codon_start=1
/transl_table=11
/product="hypothetical phage protein"
/protein_id="AAL97442.1"
/db_xref="GI:19747951"
/translation="MATELIFGVGFLAVTNTYINFNKSIKHANDITLLOSEVHL
KIVYRONARLEEHAEQNKTLITMTQIKNLTPDVLDKDMRGEIK"
6250..6477
/gene="spym18_0776"
6250..6477
/gene="spym18_0776"
/feature="best blastp match gb|AAK33662.1| (AE006522)
putative holin, phage associated [Streptococcus pyogenes
M1 GAS]"
/codon_start=1
/transl_table=11
/product="putative holin"
/protein_id="AAL97443.1"
/db_xref="GI:19747952"
/translation="MINLKLRLQNKVTLMAILGAILLAQQLGKILPSNIADIANTAV
TILVLGVYNDPPTTKGSDSEQALTYHEPK"
6593..7798
/gene="spym18_0777"
6593..7798
/gene="spym18_0777"
/feature="best blastp match gb|AAK34243.1| (AE006580)
hypothetical protein - phage associated [Streptococcus
pyogenes M1 GAS]"
/codon_start=1
/transl_table=11
/product="hypothetical phage protein"
/protein_id="AAL97444.1"
/db_xref="GI:19747953"
/translation="MIFPLDKIKGCCLDGMAKRYILPSLRAQAALIESGCKKAPPHAL
EGIKRADSMTGKSFNRTQDEYQAGVITTDVDFRAYDSWDESIADHGFVLVDPYQ
SVTGEADYKKAACHAIDAGYATASGYAEILLIQIEBNNNLOKMKKEAIVREKOMISO
CREVIEFFIILANAGMGVDDSPAGQCADVPCYAKAHMFDVLMGNALIDLDSAAV
GWEVHMPTDANPLTGAFPYQSVYHGFQGTGIVIRDSGTYMRTVEONIDGNPDALY
VGAARPENRDPFTGVMFYPRYQGTIVQPVSTEPQTSSTIYETAKTIGTFTDVAEI
NIRWPSLASSEVGSYKQGDYVSFDNEGIANGYIWLSTYVGGSGMRNTLGIQGTDKDN
RISLWGLKN"
complement(7866..8573)
/gene="spec"
/feature="synonym: spym18_0778"
complement(7866..8573)
/gene="spec"
/feature="best blastp match pirl|A30509 exotoxin C precursor
- streptococcus pyogenes"
/codon_start=1
```

```

/transl_table=11
/product="exotoxin C precursor"
/protein_id="A197445.1"
/db_xref="GI:19747954"
/translation="MKKINIKIVETITVILISTIPRIKSDSKDISNKSDDLAV
TIRPYDKDCRVNSTHTLIDFQKRGDYSSSMYSKQKRDHVDVGLF
YIINSHGEYIYGGITPAONKNVHKLGILFISGEQONNNKILERKIDVFQED
FKIRKYLMDNVKIDATSPVYSRIEIGTDGKREQDLDPSNEGSRSDIFAKYKN

```

Query Match 97.88; Score 915.2; DB 1; Length 11277;

Best Local Similarity 96.68; Pred. No. 1,8e-139;

Matches 923; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

```

QY 1 CAACCTTGACATTTAAATGAAGTGCACCTCAAAACCTAAATATTAATACATTTAT 60
Db 8726 CAACCTTGACATTTAAATGAAGTGCACCTCAAAACCTAAATATTAATACATTTAT 8667
QY 61 AAAATTTCTAAATAAAGAAATCGATTTTAACTACTACTCTATTTTCATGTTCT 120
Db 8666 AAAATTTCTAAATAAAGAAATCGATTTTAACTACTACTCTATTTTCATGTTCT 8607
QY 121 CGTACGATATACATTTAATTAAGAGAAAATGAAAAGATTACATCATCAATA 180
Db 8606 CGTACGATATACATTTAATTAAGAGAAAATGAAAAGATTACATCATCAATA 8547
QY 181 GTTTTCATTAATTCAGTCACTGATTTCTACTATTTTCACCTATCATCAAGTACTCT 240
Db 8546 GTTTTCATTAATTCAGTCACTGATTTCTACTATTTTCACCTATCATCAAGTACTCT 8487
QY 241 AAGAAGACATTTTGAATGTTAAAGATTTACTTATGCAATCACTATTAATCTCTAT 300
Db 8486 AAGAAGACATTTTGAATGTTAAAGATTTACTTATGCAATCACTATTAATCTCTAT 8427
QY 301 GATTATTAAGATTCAGGATTAATTTTCAACGACACACATTAACATTTGATGATCA 360
Db 8426 GATTATTAAGATTCAGGATTAATTTTCAACGACACACATTAACATTTGATGATCA 8367
QY 361 AAATATAGAGGAAAGACTATTAATTAATAGTTCGAAATGTTTATGAGGCTCTCAAAA 420
Db 8366 AAATATAGAGGAAAGACTATTAATTAATAGTTCGAAATGTTTATGAGGCTCTCAAAA 8307
QY 421 TTTAAAGAGATGATCATGATGATTTTGGATTTATTTATTTATTTCTTAATTCACACC 480
Db 8306 TTTAAAGAGATGATCATGATGATTTTGGATTTATTTATTTATTTCTTAATTCACACC 8247
QY 481 GGTGAGTACATCTGTGAGAGAAATACCGCTGCTCAAAATATAAGTAATATCAATATTA 540
Db 8246 GGTGAGTACATCTGTGAGAGAAATACCGCTGCTGCTCAAAATATAAGTAATATCAATATTA 8187
QY 541 TTGGGAAATCTATTTATTTGCGGGAATCTCAACAGACTTAATTAACAGATTATTTCTA 600
Db 8186 TTGGGAAATCTATTTATTTGCGGGAATCTCAACAGACTTAATTAACAGATTATTTCTA 8127
QY 601 GAAAAGATATGCGTAATCTTCCAGGAATGACTTTAAATTCAGAAATACCTATGAT 660
Db 8126 GAAAAGATATGCGTAATCTTCCAGGAATGACTTTAAATTCAGAAATACCTATGAT 8067
QY 661 AATTATTAATTTATGACGCTACTTCTCTATTAAGCGGACAGATCGAATTTGGACA 720
Db 8066 AATTATTAATTTATGACGCTACTTCTCTATTAAGCGGACAGATCGAATTTGGACA 8007
QY 721 AAAGATGGAAACATGACAAATAGACTTATTTGACTCACCAGTAAGAGGACTAGATCA 780
Db 8006 AAAGATGGAAACATGACAAATAGACTTATTTGACTCACCAGTAAGAGGACTAGATCA 7947
QY 781 GATATTTTTCGAAATTAAGAAATATGAATTAATCAATTAAGAACTTATGATTCATTC 840
Db 7946 GATATTTTTCGAAATTAAGAAATATGAATTAATCAATTAAGAACTTATGATTCATTC 7887
QY 841 GATATTTATCTTGAAAATTAATTCATCATACAAAAACCGCCAGAAATATCTGAGCG 900
Db 7886 GATATTTATCTTGAAAATTAATTCATCATACAAAAACCGCCAGAAATATCTGAGCG 7827

```

Oy 901 GTTTGCTTATCTCGAGCTTTTACTCTCTAATTTA 936
Db 7826 GTTTGCTTATCTCGAGCTTTTACTCTCTAATTTA 7791

RESULT 3

AE006523/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

10029 bp DNA Linear BCT 01-JUN-2001
Streptococcus pyogenes M1 GAS strain SF370, section 52 of 167 of
the complete genome.
AE006523 AE004092
AE006523.1 GI:13621893
Streptococcus pyogenes M1 GAS
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
1 (bases 1 to 10029)
Ferretti, J.J., McShan, W.M., Adji, D., Savic, D., Savic, G., Lyon, K.,
Primeaux, C., Sezate, S.S., Surorov, A.N., Kenton, S., Lai, H., Lin, S.,
Qian, X., Jia, H.G., Najjar, F.Z., Ren, O., Zhu, H., Song, L., White, J.,
Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.
Complete genome sequence of an M1 strain of Streptococcus pyogenes
Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
21192684
PUBMED
11296296
2 (bases 1 to 10029)
Ferretti, J.J., McShan, W.M., Adji, D., Savic, D., Savic, G., Lyon, K.,
Primeaux, C., Sezate, S.S., Surorov, A.N., Kenton, S., Lai, H., Lin, S.,
Qian, X., Jia, H.G., Najjar, F.Z., Ren, O., Zhu, H., Song, L., White, J.,
Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.
Direct Submission
Submitted (10-APR-2001) Department of Microbiology and Immunology,
University of Oklahoma Health Sciences Center, 940 St. Young Blvd.,
Oklahoma City, OK 73104, USA
Location/Qualifiers
1..10029
/organism="Streptococcus pyogenes M1 GAS"
/mol_type="genomic DNA"
/strain="SF370"
/serotype="M1"
/db_xref="taxon:160490"
1..3287
/note="bacteriophage 370.1 DNA"
89..1291
/gene="Spy0710"
89..1291
/gene="Spy0710"
/note="Best Blastp hit = pir|IT13528 hypothetical protein
39 - Bacillus phage phi-105 >g141266251dbj|BAA36645.1
(AB016282) ORF39 [bacteriophage phi-105]"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein, phage
associated"
/protein_id="AAK33663.1"
/db_xref="GI:13621894"
/translation="MPELDIKIOGCLDGMAYKILPSLTAQAALLESQMKHAPHNL
EGIKADSSWTKSEFDKTOBEYXQAGVYTDIDREPRAYDSWESIDAHGOTLNNPRE
AYIGEDYKACAIKAGATATSSIVELLIDLENDLQSWREALKNKEETMTTA
NETVOYCVNLANSNGMVDKDAHGTQCCDLPCEVANKMFEVDLMDLSDASAG
WEVHRMPTENPRAGATFYQSVYHOFGHGIVIEISDGYTMRTEQNDLGNDAV
GAPARENTRFDTGVIGWFPYQYDGYTQVSTPEQSDRIETAKGTFTLVAELN
IRMPSLASEVGVYIKGDIVSPDSSEYANGYWIWYSGSGMRNVLIGQTDKDNR
ISLWGRKLN"
complement(1359..2066)
/gene="spec"
/note="synonym: Spy0711"
complement(1359..2066)
/gene="spec"
/note="Best Blastp hit = pir|A30509 exotoxin C precursor
- Streptococcus pyogenes >g11536211gb|AAA27017.11
(M35514) streptococcal pyrogenic exotoxin type C (spec)

precursor [Streptococcus pyogenes]"
/codon_start=1
/transl_table=11
/product="pyrogenic exotoxin C precursor, phage associated"
/protein_id="AAK33664.1"
/db_xref="GI:13621895"
/translation="MKKINIKIYFITTILLISPIIISDKSKDISINYKSLDLVAY
TITPYDKKNCRVNFTHTLIDOKRGKDYISSEMSYASOKFKRDDHVGEGF
YIINSHGIEYIGGIFTPAONNKVHKILGNLFISSECOQLNKKIIEKIDIVTFOED
FKIRKYLMDNYKIDATSPYSGRIEIGTKDGKHEQIDLPDSNEGTRSDIFAKYKN
RIINMKNFSHFDIYLEK"
/complement(2177..2935)
/gene="mf2"
/note="synonym: SPY0712"
complement(2177..2935)
/gene="mf2"
/note="Best Blastp hit = sp|Q03158|NUCE_STRPN_DNA_ENTRY
NUCLEASE (COMPETENCE-SPECIFIC NUCLEASE)
>g1|98025|pir||S10641 enda protein - Streptococcus
pneumoniae >g1|47374|emb|CAA38134.1| (X54225) membrane
nuclease [Streptococcus pneumoniae]"
/codon_start=1
/transl_table=11
/product="putative DNase (similar to mitogenic factor),
phage associated"
/protein_id="AAK33665.1"
/db_xref="GI:13621896"
/translation="MKLSKOKASLITRVALLLSITTTVDARVTPYNSHANTH
YKRVSSKILLPTANYQLOJELDNLRATFSHIQODRHETKDVPRKINVDPGWN
YQPPYDGSKSSWMNRGHLVGYQFCGLNDEPRNLVMTAMLTGAYSANDSPQM
LYENRDLSDMLALHPDEWLDYKVPIYSGNEVYPRQIEIQYVIGDSGELLITRLNS
KESIDENVTVTIENSAPNINLDYLGATPKN"
3247..4665
/gene="pepd"
/note="synonym: SPY0713"
3247..4665
/gene="pepd"
/EC_number="3.4.13.18"
/note="Best Blastp hit = emb|CAA66210.1| (Z38063)
dipeptidase [Lactobacillus helveticus]"
/codon_start=1
/transl_table=11
/product="putative dipeptidase"
/protein_id="AAK33666.1"
/db_xref="GI:13621897"
/translation="MDKKIORFSCSTTILVKKKASYDGSITWARTEDSQNDFTPKMI
VVRPEDPRIHRSVQSFEMDLDPNEMTVTVSVPALDKDGIWAGVNEANWASAVE
TITNSKVLADAPLVASGIEEDMVLVIRPARGVLRGAILDEYGEESGVA
FSDEHDIMLETTIGGHHIARVPDDAYVTPNQFGIDHEFNPEDEYLCADLKDFI
DYHLDLTYSHENPRYAFSGORNDKROYNTPRAMTOKELFNEIYQDPSFALAMC
OKPRKTTVEDEVKVLSSHYODGYDPSGSEGVSKVFRPIGINRTSOTAILHIP
NKPOETAIQOMAVYGSMPNTMVPFTQVKTIPDYKANTYENFTDNPFTYTRILIAL
ADPHYNHETDLDYLETMAKGHAMLAHEVOLLAGEITVLEENQKMSDYVGETO
TLNKLILEASNLMTNRFSLSD"
3271..3287
/gene="pepd"
/note="bacteriophage 370.1 - attp-L"
4817..6364
/gene="adca"
/note="synonym: SPY0714"
4817..6364
/gene="adca"
/note="Best Blastp hit = emb|CAA96185.1| (Z71552) Adca
protein [Streptococcus pneumoniae]"
/codon_start=1
/transl_table=11
/product="putative adhesion protein"
/protein_id="AAK33667.1"
/db_xref="GI:13621898"
/translation="MKKKIILMSLISVFAWOLTOAKOYLAEKQVAVVTFPYEEF
TKGVIGDGVFMLKAGTEPHDEPSTKIKIQQADAVVIMDNNEITWSDVKSL
TSKVTYIKGTGNMLVAAGAHDBPHEDADKHEHNHSEGHNAHDPHVLSPYRS

ITVENIRDSLKAYPEKAENFKANATYIEKLEKDELDKYTAALSDAKOKSFYTHAA
EGYMALDYGLNOLISINCVTDDAPSAKRIATPLSKYVKKYGIKYIEEMNSVAKTL
AKEGVAAVLNLSPLEGLTEKEMKAGOGYFPMVRKNLETLLETDVACKELLPEKDTK
TVYNGYFKDKVEKDRQLSDNSGWSQYVPLQDSTLDQVMDYKAKSKGKMTAEYKD
YTTGYKTDVEQIKINGRKRTMTFVRNGEKRTFTYTAGKEILITPYPGNNGVRFMEFA
KADAGEFKYVOFSDBAIAPEKAKHFLYMGDSQSEKILKLEHWPYVYSGDSIGREI
AOEINAH"
6512..7234
/gene="SPY0715"
6512..7234
/gene="SPY0715"
/note="Best Blastp hit = db|JBA04138.1| (AP001508)
transcriptional regulator (GntR family) [Bacillus
halodurans]"
/codon_start=1
/transl_table=11
/product="putative transcriptional regulator (GntR
family)"
/protein_id="AAK33668.1"
/db_xref="GI:13621899"
/translation="MPKEOPLVYQIYNDLEFKIKKSMENDKILSEBELSDIGVSRIT
TRITLKELELRDLITKKQKGYVSGIKEPAYDLSSTYFTEDMKMKGTPTKEIIS
FEQYQVTPYLSGLELDPDTEVELELERLRADMPLEFASYPAPQFQSLADLKR
KALYDIPAKDYQETIRLAEBEFYASIALDYEAGLIGIKGDPVLHITRKTYNDKNILI
ELRFSIARADQFRYVOHHPNG"
7253..8452
/gene="agas"
7253..8452
/note="synonym: SPY0716"
7253..8452
/gene="agas"
/note="Best Blastp hit = sp|P42907|AGAS_ECOLI PUTATIVE
NAGATOSE-6-PHOSPHATE KETOSE/ALDOSE ISOMERASE
tagatose-6-phosphate hit = sp|P42907|AGAS_ECOLI PUTATIVE
>g1|7465773|pir||D65103 agas protein - Escherichia coli
(strain K-12) >g1|60607|gb|J014A57939.1| (U018997) ORE_C384
[Escherichia coli] >g1|1789525|gb|AAC76170.1| (AE000395)
putative tagatose-6-phosphate aldose/ketose isomerase
[Escherichia coli]"
/codon_start=1
/transl_table=11
/product="putative tagatose-6-phosphate aldose/ketose
isomerase"
/protein_id="AAK33669.1"
/db_xref="GI:13621900"
/translation="MPTKTOALEALGAITTKERIKOEPRLMOETMFEFETRSLDS
FKIKVCSANRNVHVFETGAGTSEYIGNITCPYKGVGRORLPFSVSTDLVAP
DYIYVEEYVLVLSFARSGSPESVAAYNVNQLVPVSHITLITKADGELAKAQOD
ERSTLYLMPEDANDAGFAMTGSFTCMALALITFDDNSIAOKFAVYTDMLAQAVT
DOERRLOELADLGEERLVYIGSAGLALITQEOALKMLKELTAGOVATYEFSEMGRRP
KSFINDRTLVYIGFVNNDAYVROYDLMLETOADGIALKELTIALOGGDINSEDOFRL
DTRILLDPAIAFPMIIVAOITLALTFRVTLGNSPDPSANGTVARVYKVTIHPYPS
SROCNKA"
complement(8549..8809)
/gene="rpbm"
/note="synonym: SPY0717"
complement(8549..8809)
/gene="rpbm"
/note="Best Blastp hit = sp|Q92H28|RLJ1_LISMO 50S
RIBOSOMAL PROTEIN L31"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L31"

Query Match 97.3%: Score 910.4; DB 1; Length 10029;
Best Local Similarity 98.3%: Pred. No. 1.1e-138;
Matches 920; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 1 CAACCTTGACATTTAAATGGAAGTCCACCTCTAAAGCTAAATATTAATACATTAT 60
|||||
DB 2219 CAACCTTGACATTTAAATGGAAGTCCACCTCTAAAGCTAAATATTAATACATTAT 2160
|||||
OY 61 AAAATTTCTAATAAGAGAAATCTGATTTTAACTACTAGCTGATTTTCATGATCT 120
|||||
DB 2159 AAAATTTCTAATAAGAGAAATCTGATTTTAACTACTAGCTGATTTTCATGATCT 2100
|||||

Accession	Source	Organism	Reference
121	CGTACGATATACATTTAAATTAAGAGGAA	Staphylococcus aureus	1
2099	CGTACGATATACATTTAAATTAAGAGGAA	Staphylococcus aureus	2
181	GTTCATCAATTAACAGTATACATTTAAAT	Staphylococcus aureus	3
2039	GTTCATCAATTAACAGTATACATTTAAAT	Staphylococcus aureus	4
241	AAGAAACATTTGCAATGTTAAAGATGTT	Staphylococcus aureus	5
1979	AAGAAACATTTGCAATGTTAAAGATGTT	Staphylococcus aureus	6
301	GATTATTAAGATTCGAGGCTAAATTTTTC	Staphylococcus aureus	7
1919	GATTATTAAGATTCGAGGCTAAATTTTTC	Staphylococcus aureus	8
361	AAATATAGAGGAAAGACTATTTATTAAT	Staphylococcus aureus	9
1859	AAATATAGAGGAAAGACTATTTATTAAT	Staphylococcus aureus	10
421	TTTAAGAGATGATCATGTGATGTTTGAT	Staphylococcus aureus	11
1799	TTTAAGAGATGATCATGTGATGTTTGAT	Staphylococcus aureus	12
481	GGTGGATCATCTATGAGGAAATTAAGCT	Staphylococcus aureus	13
1739	GGTGGATCATCTATGAGGAAATTAAGCT	Staphylococcus aureus	14
541	TTGGGAAATCTATTTATTTTCGGGAAAT	Staphylococcus aureus	15
1679	TTGGGAAATCTATTTATTTTCGGGAAAT	Staphylococcus aureus	16
601	GAAAGATATCGTACCTTTCCAGGAAAT	Staphylococcus aureus	17
1619	GAAAGATATCGTACCTTTCCAGGAAAT	Staphylococcus aureus	18
661	AATATTAATTTATGACGCTCTTCCTAT	Staphylococcus aureus	19
1559	AATATTAATTTATGACGCTCTTCCTAT	Staphylococcus aureus	20
721	AAAGATGGGAAACATGAGCAATATGACT	Staphylococcus aureus	21
1499	AAAGATGGGAAACATGAGCAATATGACT	Staphylococcus aureus	22
781	GATATTTTTCGAAATTAAGATTAATGAT	Staphylococcus aureus	23
1439	GATATTTTTCGAAATTAAGATTAATGAT	Staphylococcus aureus	24
841	GATATTTATCTTGAAGAAATTAATGAT	Staphylococcus aureus	25
1379	GATATTTATCTTGAAGAAATTAATGAT	Staphylococcus aureus	26
901	GTTCATCAATTAACAGTATACATTTAA	Staphylococcus aureus	27
1319	GTTCATCAATTAACAGTATACATTTAA	Staphylococcus aureus	28

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT	FEATURES	source	gene	CDS
88314303	3045005	2 (bases 1 to 702)	Kapur,V., Nelson,K., Schleifert,P.M., Selaender,R.K. and Musser,J.M							
			Molecular population genetic evidence of horizontal spread of two alleles of the pyrogenic exotoxin C gene (spec) among pathogenic clones of Streptococcus pyogenes							
			Infect. Immun. 60 (9), 3513-3517 (1992)							
			92363541							
			1500157							
			Original source text: Streptococcus pyogenes (library: MGAS 1251) DNA.							
			Location/Qualifiers							
			1..702							
			/organism="Streptococcus pyogenes"							
			/mol_type="genomic DNA"							
			/db_xref="taxon:1314"							
			/tissue_lib="MGAS 1251"							
			1..702							
			/gene="pyrogenic exotoxin C"							
			1..>702							
			/gene="pyrogenic exotoxin C"							
			/function="pyrogenic exotoxin superantigen"							
			/codon_start=1							
			/transl_table=11							
			/product="pyrogenic exotoxin C"							
			/protein_id="AAB59091.1"							
			/db_xref="GI:153785"							
			/translation="MKKNTIKYFITVILISITSPKSDSKKDISNKSLLIYAM							
			TIITPKDKRVNFTSTHTLIDPQKRYKDYISSEMSYASQFKRDHVDVGLT							
			YLINSHGEYIYGGITPAQNNKVNHLKGLNFISGE500LNKKIIEKDIYTOEID							
			EIKRIYLMNDNRYKIDATSPYSGRIEIGTKDGHQIDLPDSPNEGTRSDIFARYKDD							
			RIIMKNFSHEDYLE"							
			1..81							
			/gene="pyrogenic exotoxin C"							
			82..>702							
			/gene="pyrogenic exotoxin C"							
			/product="pyrogenic exotoxin C"							
			/function="pyrogenic exotoxin superantigen"							
			61..78							
			/gene="pyrogenic exotoxin C"							
			/citation=11							
			/replace="tattcactcatcatca"							
			/ORIGIN							
			BASE COUNT							
			274 a 101 c 103 g 224 t							
			Query Match							
			Best Local Similarity 98.1%; Pred. NO. 3.1e-101;							
			Matches 689; Conservative 0; Mismatches 13; Indels 0; Gaps 0;							
			154 ATGAAAAGATTACATCATCAAAATAGTTTCATATTTACAGTCATCTGATTTCTACT							
			1 ATGAAAAGATTACATCATCAAAATAGTTTCATATTTACAGTCATCTGATTTCTACT							
			214 TATTTACACCTTACATCAAAAGTACCTCTAAGAAAGCATTTGGAAATGTAAGCATTTA							
			61 ATTTCACCTTACATCAAAAGTACCTCTAAGAAAGCATTTGGAAATGTAAGCATTTA							
			274 CTTATGACATACACTATTAACCTCTTATGATTATAAAGATTCAGAGGTAAATTTTCAACG							
			121 CTTATGACATACACTATTAACCTCTTATGATTATAAAGATTCAGAGGTAAATTTTCAACG							
			334 ACACACACATTAACATGATTAACCTCTAAGAAAGCATTTATTAATTAAGTTC							
			181 ACACACACATTAACATGATTAACCTCTAAGAAAGCATTTATTAATTAAGTTC							
			394 GAAATGCTTATGAGGCGCTCAAAAATTTAAGAGATGATCATGATGATGATTTTGG							
			241 GAAATGCTTATGAGGCGCTCAAAAATTTAAGAGATGATCATGATGATGATTTTGG							
			454 TTATTTTATATTTCTTAAATTTCTACACCGGTGATCATCTATGAGAAATTAAGCGTCT							
			301 TTATTTTATATTTCTTAAATTTCTACACCGGTGATCATCTATGAGAAATTAAGCGTCT							

```

OY 514 CAAATPATAAGTAATCATATATTTGGAAATCTATTTTCGGAGATCCAA 573
    |||||||
Db 361 CAAATATATAAGTAATCATATATTTGGAAATCTATTTTCGGAGATCCAA 420
OY 574 CAGAACTTAATAACAAGATTTATCTAGAAAAGATATCTTAACCTTCCAGAAATTCAC 633
    |||||||
Db 421 CAGAACTTAATAACAAGATTTATCTAGAAAAGATATCTTAACCTTCCAGAAATTCAC 480
OY 634 TTTAAATTCAGAAATTCCTTATGATATTAATAATTTATGACGCTACTTCCCTTAT 693
    |||||||
Db 481 TTTAAATTCAGAAATTCCTTATGATATTAATAATTTATGACGCTACTTCCCTTAT 540
OY 694 GTAGCGCGAGAAATTCGAAATTTGGCACAAGATGGGAAATGACCAATAGACTTATTT 753
    |||||||
Db 541 GTAGCGCGAGAAATTCGAAATTTGGCACAAGATGGGAAATGACCAATAGACTTATTT 600
OY 754 GACTCACCAGAAATGAGGAGCTAGATCAGATATTTTTCGCAAAATATAAGATTAATAGATT 813
    |||||||
Db 601 GACTCACCAGAAATGAGGAGCTAGATCAGATATTTTTCGCAAAATATAAGATTAATAGATT 660
OY 814 ATCAATATGAAAGAACTTATGATTCATTTGATATTTATCTTGAA 855
    |||||||
Db 661 ATCAATATGAAAGAACTTATGATTCATTTGATATTTATCTTGAA 702

RESULT 5
STREPEXC 702 bp DNA linear BCT 26-Apr-1993
LOCUS Streptococcus pyogenes pyrogenic exotoxin C gene, 5' end cds.
DEFINITION M97157
VERSION M97157.1 GI:153786
KEYWORDS pyrogenic exotoxin C; superantigen.
SOURCE Streptococcus pyogenes
ORGANISM Streptococcus pyogenes
REFERENCE 1 (sites)
AUTHORS Goshorn,S.C. and Schlievert,P.M.
TITLE Nucleotide sequence of streptococcal pyrogenic exotoxin type C
JOURNAL Infect. Immun. 56 (9), 2518-2520 (1988)
MEDLINE 88314303
PUBMED 3045005
2 (bases 1 to 702)
REMARKS Kapur,V., Nelson,K., Schlievert,P.M., Selander,R.K. and Musser,J.M.
REFERENCE Molecular population genetic evidence of horizontal spread of two
AUTHORS alleles of the pyrogenic exotoxin C gene (spec) among pathogenic
TITLE clones of Streptococcus pyogenes
JOURNAL Infect. Immun. 60 (9), 3513-3517 (1992)
MEDLINE 92363541
PUBMED 1500157
COMMENT Original source text: Streptococcus pyogenes (library: MGAS 332)
DNA.

FEATURES
source
    Location/Qualifiers
        1..702
            /organism="Streptococcus pyogenes"
            /mol_type="genomic DNA"
            /db_xref="taxon:1314"
            /tissue_lib="MGAS 332"
        1..702
            /gene="pyrogenic exotoxin C"
        1..>702
            /gene="pyrogenic exotoxin C"
            /function="pyrogenic exotoxin C"
            /function="pyrogenic exotoxin superantigen"
            /transl_table=1
            /codon_start=1
            /product="pyrogenic exotoxin C"
            /protein_id="AAB59092.1"
            /db_xref="GI:153787"
            /translation="MKKINIKIVFITVLLISTIPISDSKDISNKSLLIAY
            TTPYDKDCRVNFTSTHTIDPQKRGKDYISSMSYEAQOKERDHDVFGLE
            YIINSHGEVYIGGIIIPAONNNKVLHKLGLFTSGESQQLNNKIIILEKDIIVFOED
            FKIRKYLMDNYKIVDATSPPVSGRIEIGTKDKHQEQIDLPSPNEGTRSDIFAKYKDN"

gene
CDS
```

```

RIIMKNFSHFIDYLE"
sig_peptide 1..81
/gene="pyrogenic exotoxin C"
mat_peptide 82..>702
/gene="pyrogenic exotoxin C"
/product="pyrogenic exotoxin C"
/function="pyrogenic exotoxin superantigen"
conflict 61..78
/gene="pyrogenic exotoxin C"
/citation="(1)
/replace="tattcaccatcatca"
BASE COUNT 276 a 101 c 101 g 224 t
ORIGIN
Query Match 72.48; Score 678; DB 1; Length 702;
Best Local Similarity 97.98; Pred. No. 1e-100;
Matches 687; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 154 ATGAAAAGATTTAATCATATCAAAATAGTTTCTAATTTACAGTCATGATTTCTACT 213
    |||||||
Db 1 ATGAAAAGATTTAATCATATCAAAATAGTTTCTAATTTACAGTCATGATTTCTACT 60
OY 214 TATTTACCTATCATCAAAAGTACTCTAAGAAACATTTGCAATGTTAAAGTATTA 273
    || |
Db 61 ATTTCACCTATCATCAAAAGTACTCTAAGAAACATTTGCAATGTTAAAGTATTA 120
OY 274 CTTTATGCTATACATATTAATCTCTTATGATTTATTAACATTTGACGGTAAATTTTTCACG 333
    |||||||
Db 121 CTTTATGCTATACATATTAATCTCTTATGATTTATTAACATTTGACGGTAAATTTTTCACG 180
OY 334 ACACACATTTAATCATTTGATCTCAAAATATATGAGGAAAGCATTTATTTAGTTCC 393
    |||||||
Db 181 ACACACATTTAATCATTTGATCTCAAAATATATGAGGAAAGCATTTATTTAGTTCC 240
OY 394 GAAATGCTTATGAGGCTCTCAAAATTTAAACGAGATGATCATGATGTTTTTGA 453
    |||||||
Db 241 GAAATGCTTATGAGGCTCTCAAAATTTAAACGAGATGATCATGATGTTTTTGA 300
OY 454 TTATTTTATTTCTTATTTCTCACACCGGAGTACATCTATGAGGAATTTACCGCTGCT 513
    |||||||
Db 301 TTATTTTATTTCTTATTTCTCACACCGGAGTACATCTATGAGGAATTTACCGCTGCT 360
OY 514 CAAATATATAAGTAATCATATTAATTTTGGGAATCTATTTATTTGGGAGATCCAA 573
    |||||||
Db 361 CAAATATATAAGTAATCATATTAATTTTGGGAATCTATTTATTTGGGAGATCCAA 420
OY 574 CAGAACTTAATAACAAGATTTATCTAGAAAAGATATCTTAACCTTCCAGAAATTCAC 633
    |||||||
Db 421 CAGAACTTAATAACAAGATTTATCTAGAAAAGATATCTTAACCTTCCAGAAATTCAC 480
OY 634 TTTAAATTCAGAAATTCCTTATGATATTAATAATTTATGACGCTACTTCCCTTAT 693
    |||||||
Db 481 TTTAAATTCAGAAATTCCTTATGATATTAATAATTTATGACGCTACTTCCCTTAT 540
OY 694 GTAGCGCGAGAAATTCGAAATTTGGCACAAGATGGGAAATGACCAATAGACTTATTT 753
    |||||||
Db 541 GTAGCGCGAGAAATTCGAAATTTGGCACAAGATGGGAAATGACCAATAGACTTATTT 600
OY 754 GACTCACCAGAAATGAGGAGCTAGATCAGATATTTTTCGCAAAATATAAGATTAATAGATT 813
    |||||||
Db 601 GACTCACCAGAAATGAGGAGCTAGATCAGATATTTTTCGCAAAATATAAGATTAATAGATT 660
OY 814 ATCAATATGAAAGAACTTATGATTCATTTGATATTTATCTTGAA 855
    |||||||
Db 661 ATCAATATGAAAGAACTTATGATTCATTTGATATTTATCTTGAA 702

RESULT 6
SP002559 619 bp DNA linear BCT 30-Jan-2001
LOCUS Streptococcus pyogenes spec gene, partial cds.
DEFINITION U02559
ACCESSION U02559.1 GI:409024
VERSION
```

```
KEYWORDS
SOURCE      Streptococcus pyogenes
ORGANISM    Streptococcus pyogenes
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1 (bases 1 to 619)
AUTHORS    Norrby-Teglund,A., Holm,S.E. and Norgren,M.
TITLE      Detection and nucleotide sequence analysis of the spec gene in
            Swedish clinical group A streptococcal isolates
JOURNAL     J. Clin. Microbiol. 32 (3), 705-709 (1994)
MEDLINE     94253335
PUBMED      8195383
REFERENCE   2 (bases 1 to 619)
AUTHORS    Norrby-Teglund,A.
TITLE      Direct Submission
JOURNAL     Submitted (17-OCT-1993) Anna Norrby-Teglund, University of Umea,
            Clinical Bacteriology, Umea S-901 85, Sweden
FEATURES
Source      1..619
            /organism="Streptococcus pyogenes"
            /mol_type="genomic DNA"
            /strain="NY5"
            /db_xref="taxon:1314"
            /clone="spec"
            <1..>619
            /gene="spec"
            <1..>619
            /codon_start=1
            /transl_table=11
            /protein_id="AAB59977.2"
            /db_xref="GI:12597942"
            /translation="ISPIKSDSKDISNVKSDLLVATITPYDKDCRVNFTHTL
            NIDQKRGKDYIISSEYASQKFRKRDYVFGLEFYILNSHTGEIYIGITPAON
            NKNVHKILGNLFISGESQONLNKIIILEKDIYVFOEDFKIRKILMNKIKYIDATSPY
            VSGRIEIGTKDGRKHEQIDLPDSNEGTRSDIFAKYKDNRIINKNF"
            87
            /gene="spec"
            /replace="t"
            90 c          93 g          191 t

BASE COUNT      245 a          90 c          93 g          191 t
ORIGIN
Query Match      64.3%; Score 602.2; DB 1; Length 619;
Best Local Similarity 99.4%; Pred. No. 2.1e-88;
Matches 615; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY      215 ATTACCTATCATC-AAAGTGACTCTAAGAAAGACATTTGAGATGTTAAAGCATTTA 273
            |||||||
DB      1 ATTACCTATCATCAAAAGTCAAGACTCTAAGAAAGACATTTGAGATGTTAAAGCATTTA 60
QY      274 CTTATGCAATACATTAACCTCTTATGATTAATTAAGATTGACAGGTAATTTTCAACG 333
            |||||||
DB      61 CTTATGCAATACATTAACCTCTTATGATTAATTAAGATTGACAGGTAATTTTCAACG 120
QY      334 ACACACACATTAAACATTGATCTCAAAAATATAGAGGAAAGACTATTATATTAGTTCC 393
            |||||||
DB      121 ACACACACATTAAACATTGATCTCAAAAATATAGAGGAAAGACTATTATATTAGTTCC 180
QY      394 GAATGCTTATAGGGCCTCTCAAAAATTTTAAAGAGATGTCATGTAGATGTTTGGGA 453
            |||||||
DB      181 GAATGCTTATAGGGCCTCTCAAAAATTTTAAAGAGATGTCATGTAGATGTTTGGGA 240
QY      454 TTATTTATATCTTAAATCTCACACCGGAGTACATCTATGGAGAAATAGCCCTGCT 513
            |||||||
DB      241 TTATTTATATCTTAAATCTCACACCGGAGTACATCTATGGAGAAATAGCCCTGCT 300
QY      514 CAAAATAATAAGTAATCATTAATTTATGGGAATCTATTTTGGGAGAAATCTCAA 573
            |||||||
DB      301 CAAAATAATAAGTAATCATTAATTTATGGGAATCTATTTTGGGAGAAATCTCAA 360
QY      574 CAGACTTAATAATCAAGATTATCTAGAAAAGATATCGTAACCTTCCAGGAATTTGAC 633
            |||||||
DB      361 CAGACTTAATAATCAAGATTATCTAGAAAAGATATCGTAACCTTCCAGGAATTTGAC 420
```

```
QY      634 TTAAATCAGAAATACCTTAGATTAATTATAAATTTATGACGCTACTTCCTTAT 693
            |||||||
DB      421 TTAAATCAGAAATACCTTAGATTAATTATAAATTTATGACGCTACTTCCTTAT 480
QY      694 GTAAGCGGAGAAATGGAATTTGGCACAAGATGGAACATGAGCAAAATAGACTTATTT 753
            |||||||
DB      481 GTAAGCGGAGAAATGGAATTTGGCACAAGATGGAACATGAGCAAAATAGACTTATTT 540
QY      754 GACTCACCAGTAATGAGGACATGATCATATTTTTCGCAAAATATAAGATAATGAAAT 813
            |||||||
DB      541 GACTCACCAGTAATGAGGACATGATCATATTTTTCGCAAAATATAAGATAATGAAAT 600
QY      814 ATCAATATGAGAACTTTA 832
            |||||||
DB      601 ATCAATATGAGAACTTTA 619

RESULT 7
SPU02560      619 bp      DNA      Linear      BCT 30-JAN-2001
LOCUS      Streptococcus pyogenes TIM1 isolate Swe88 spec gene, partial cds.
DEFINITION      U02560
ACCESSION      U02560
VERSION      U02560.1
KEYWORDS      GI:409110
SOURCE      Streptococcus pyogenes
            Streptococcus pyogenes
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1 (bases 1 to 619)
AUTHORS    Norrby-Teglund,A., Holm,S.E. and Norgren,M.
TITLE      Detection and nucleotide sequence analysis of the spec gene in
            Swedish clinical group A streptococcal isolates
JOURNAL     J. Clin. Microbiol. 32 (3), 705-709 (1994)
MEDLINE     94253335
PUBMED      8195383
REFERENCE   2 (bases 1 to 619)
AUTHORS    Norrby-Teglund,A.
TITLE      Direct Submission
JOURNAL     Submitted (17-OCT-1993) Anna Norrby-Teglund, University of Umea,
            Clinical Bacteriology, Umea S-901 85, Sweden
FEATURES
Source      1..619
            /organism="Streptococcus pyogenes"
            /mol_type="genomic DNA"
            /strain="TIM1"
            /isolate="Swe88"
            /db_xref="taxon:1314"
            /clone="spec"
            <1..>619
            /gene="spec"
            <1..>619
            /codon_start=1
            /transl_table=11
            /protein_id="AAB59978.2"
            /db_xref="GI:12597943"
            /translation="ISPIKSDSKDISNVKSDLLVATITPYDKNCRVNFTHTL
            NIDQKRGKDYIISSEYASQKFRKRDYVFGLEFYILNSHTGEIYIGITPAON
            NKNVHKILGNLFISGESQONLNKIIILEKDIYVFOEDFKIRKILMNKIKYIDATSPY
            VSGRIEIGTKDGRKHEQIDLPDSNEGTRSDIFAKYKDNRIINKNF"
            97
            /gene="spec"
            /replace="g"
            89 c          92 g          192 t

BASE COUNT      246 a          89 c          92 g          192 t
ORIGIN
Query Match      64.3%; Score 602.2; DB 1; Length 619;
Best Local Similarity 99.4%; Pred. No. 2.1e-88;
Matches 615; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY      215 ATTACCTATCATC-AAAGTGACTCTAAGAAAGACATTTGAGATGTTAAAGCATTTA 273
            |||||||
```


Db	1	ATTTCACCTTTCATCAAGAAAGGACTCTTAGAAGACATTTGCGAATGTTAAAGCATTTTA	60
Qy	274	CTTTATGCATACACTATTAATCTCTTATGATTTATTAAGATTGACAGGTAAATTTTTCACG	333
Db	61	CTTTATGCATACACTATTAATCTCTTATGATTTATTAAGATTGACAGGTAAATTTTTCACG	120
Qy	334	ACACACACATTAACATTTGATTAATCTCAAAATTTATGAGGGAAGAGCTTTTATATAGTTC	393
Db	121	ACACACACATTTAAACATTTGATTAATCTCAAAATTTATGAGGGAAGAGCTTTTATATAGTTC	180
Qy	394	GAATATGCTTATGAGGCTCTCAAAAATTTTAAACGAGATGATCATGTAGATGTTTTTGA	453
Db	181	GAATATGCTTATGAGGCTCTCAAAAATTTTAAACGAGATGATCATGTAGATGTTTTTGA	240
Qy	454	TTATTTTATATCTTAAATTTCTCACCGCGTGATCATCTATGAGGAATTAAGCGCTCT	513
Db	241	TTATTTTATATCTTAAATTTCTCACCGCGTGATCATCTATGAGGAATTAAGCGCTCT	300
Qy	514	CAAAATATATAGTAATTAATTAATTTTGGGAATCTATTTATTTGGGGAATTCGCA	573
Db	301	CAAAATATATAGTAATTAATTAATTTTGGGAATCTATTTATTTGGGGAATTCGCA	360
Qy	574	CAGAACTTAAATTAACAAGATTTATCTAGAAAAGATATCGTAACCTTCCAGGAATTCAC	633
Db	361	CAGAACTTAAATTAACAAGATTTATCTAGAAAAGATATCGTAACCTTCCAGGAATTCAC	420
Qy	634	TTTAAATTCAGAAATTAACCTTATGATTAATTAATTAATTTATGACGCTACTTCTCTAT	693
Db	421	TTTAAATTCAGAAATTAACCTTATGATTAATTAATTAATTTATGACGCTACTTCTCTAT	480
Qy	694	GTAAGCGGAGAAATTCGAAATTTGGCAAAAGATGGGAACCTTGCAAAATAGACTTATTT	753
Db	481	GTAAGCGGAGAAATTCGAAATTTGGCAAAAGATGGGAACCTTGCAAAATAGACTTATTT	540
Qy	754	GACTCACCAATTAAGAGGACTAGATGATTTTTCACAAATATTAAGATTAATAGAAAT	813
Db	541	GACTCACCAATTAAGAGGACTAGATGATTTTTCACAAATATTAAGATTAATAGAAAT	600
Qy	814	ATCAATATGAAGAATCTTGA 832	
Db	601	ATCAATATGAAGAATCTTGA 619	
RESULT 8			
LOCUS	AF055699	467 bp DNA linear BCT 22-AUG-2000	
DEFINITION	Streptococcus pyogenes exotoxin C (spec) gene, spec3 allele, partial cds.		
ACCESSION	AF055699		
VERSION	AF055699.1	GI:4206379	
KEYWORDS			
SOURCE	Streptococcus pyogenes		
ORGANISM	Streptococcus pyogenes		
REFERENCE	Bacteria: Filicutes; Lactobacillales; Streptococcaceae; Streptococcus.		
AUTHORS	1 (bases 1 to 467) Bessen,D.E., Izzo,M.W., Fiorentino,T.R., Carling,R.M., Hollingshead,S.K. and Beall,B.		
TITLE	Genetic linkage of exotoxin alleles and emm gene markers for tissue tropism in group A streptococci		
JOURNAL	J. Infect. Dis. 179 (3), 627-636 (1999)		
MEDLINE	99137798		
PUBMED	9952369		
REFERENCE	2 (bases 1 to 467) Bessen,D.E., Izzo,M.W., Fiorentino,T.R., Carling,R.M., Hollingshead,S.K. and Beall,B.		
AUTHORS	Direct Submission		
TITLE	Submitted (27-Mar-1998) Epidemiology & Public Health, Yale University School of Medicine, 333 Cedar Street, Box 208034, New Haven, CT 06520, USA		
JOURNAL			
FEATURES	Location/Qualifiers		
SOURCE	1..467		
	/organism="Streptococcus pyogenes"		

		/mol_type="genomic DNA"	
		/strain="1RP278"	
gene		/db_xref="taxon:1314"	
		<1..>467	
		/gene="spec"	
CDS		/allele="spec3"	
		<1..>467	
		/gene="spec"	
		/codon_start=1	
		/transl_table=11	
		/product="exotoxin C"	
		/protein_id="AAD11625.1"	
		/db_xref="GI:4206380"	
		/translation="-SNKSDILAVYTTTPDYKDQRNVESTHILNIDOTOKRYKKDY ISSSEASQEKFERDHDVDFGLFYLNSHTGEYIYGITPAANNVNKLGNLFI SGEQQQLNNKIIEKDIIVFOELDFIRRLMDNKYIKDPATSEVYSGRLEIGT"	
BASE COUNT	177 a	70 c	70 g 150 t
ORIGIN			
Query Match	49.4%:	Score 462.2;	DB 1; Length 467;
Best Local Similarity	99.4%:	Pred. No. 1.2e-65;	
Matches 464:	Conservative	0; Mismatches 3;	Indels 0; Gaps 0;
QY	253	TGCAATGTAAAGATGAATTACTTTATGCATACACTAATCTCTTAATGATTATAAGAT	312
Dd	1	TCGATGTGTTAAAGTGATTTACTTTATGATACACTATAACTCTTAGCATTTAAAGAT	60
QY	313	TGCAGGGTAAATTTTTTACAAGCAGACAGACATTAAACATTGATCTCAAAAATATAGAGG	372
Dd	61	TGCAGGGTAAATTTTTTACAAGCAGACAGACATTAAACATTGATCTCAAAAATATAGAGG	120
QY	373	AAGACTATTATATTAGTCCGGAATGCTTTATAGGCCCTCTCAAAAATTTAAACGAGAT	432
Dd	121	AAAGACTATTATATTAGTCCGGAATGCTTTATAGGCCCTCTCAAAAATTTAAACGAGAT	180
QY	433	GATCATGAGATGTTTTTGGATTTATTTATATTCCTAATTCACACCGGTGATACATC	492
Dd	181	GATCATGAGATGTTTTTGGATTTATTTATATTCCTAATTCACACCGGTGATACATC	240
QY	493	TATGAGAGAAATTACCGCTGCTCAAAATTAATTAATCATTAATTTATGGAGAACTCA	552
Dd	241	TATGAGAGAAATTACCGCTGCTCAAAATTAATTAATCATTAATTTATGGAGAACTCA	300
QY	553	TTTATTTTGGGAGAATCTCAACAGACTTAAATTAACAGATTATTTCTAGAAAGATATC	612
Dd	301	TTTATTTTGGGAGAATCTCAACAGACTTAAATTAACAGATTATTTCTAGAAAGATATC	360
QY	613	GTACTTTCGCGAATTTGACTTTAAATTCGAAAAATTAACCTTATGSAATTAATTAAT	672
Dd	361	GTAACCTTTCGCGAATTTGACTTTAAATTCGAAAAATTAACCTTATGSAATTAATTAAT	420
QY	673	TATACGCTACTCTCTCTTATGTAAGCGGCGAATCGAATTTGGCAC	719
Dd	421	TATACGCTACTCTCTCTTATGTAAGCGGCGAATCGAATTTGGCAC	467
RESULT 9			
AF055700	467 bp	DNA	linear BCT 22-AUG-2000
LOCUS			
DEFINITION	Streptococcus pyogenes exotoxin C (spec) gene, spec4 allele,		
ACCSSION	Partial cds.		
VERSION	AF055700		
KEYWORDS	AF055700.1 GI:4206381		
SOURCE			
ORGANISM	Streptococcus pyogenes		
REFERENCE	Streptococcus pyogenes		
AUTHORS	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.		
TITLE	1 (bases 1 to 467) Bessen,D.E., Izzo,M.W., Fiorentino,T.R., Carlingal,R.M., Hollingshead,S.K. and Beall,B. Genetic linkage of exotoxin alleles and emm gene markers for tissue tropism in group A streptococci		

JOURNAL J. Infect. Dis. 179 (3), 627-636 (1999)
 MEDLINE 99137798
 PUBMED 9952369
 REFERENCE 2 (bases 1 to 467)
 AUTHORS Bessen, D.E., Izzo, M.W., Florentino, T.R., Carling, R.M., Hollingshead, S.K. and Beall, B.
 TITLE Direct Submission
 JOURNAL Submitted (27-MAR-1998) Epidemiology & Public Health, Yale University School of Medicine, 333 Cedar Street, Box 208034, New Haven, CT 06520, USA

FEATURES
 source Location/Qualifiers
 1. 467
 /organism="Streptococcus pyogenes"
 /mol_type="genomic DNA"
 /strain="D976"
 /db_xref="taxon:1314"
 <1..>467
 /gene="spec"
 /allele="spec4"
 <1..>467
 /gene="spec"
 /codon_start=1
 /transl_table=11
 /product="exotoxin C"
 /protein_id="AADI1626.1"
 /db_xref="GI:4206382"
 /translation="SNVKSLLVATTPYDKNCRVNFTHTLNDTQYRKDY
 ISSEMSYASOKFRKRDHVDVFGFLYILNSHTGTYIGTIPADNNKYNHKLGLFI
 SGESEOONNNKILIEKDIIVTFOEIDFKIRKYLMDNRYKIYDATSPYVSGRIEIGT"

CDS
 gene
 CDS

BASE COUNT 178 a 69 c 69 g 151 t

ORIGIN

Query Match 49.4%; Score 462.2; DB 1; Length 467;
 Best Local Similarity 99.4%; Pred. No. 1.2e-65;
 Matches 464; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

OY 253 TCGAATGTTAAAGATTTACTTATGCAATACATACTCCTTATGATTATAAGAT 312
Db 1 TCGAATGTTAAAGATTTACTTATGCAATACATACTCCTTATGATTATAAGAT 60
OY 313 TGCAGGGTAAATTTTTCACAGCACACACATTAAACATTGATTCACAAAATATAGAGG 372
Db 61 TGCAGGGTAAATTTTTCACAGCACACACATTAAACATTGATTCACAAAATATAGAGG 120
OY 373 AAAGACTTTATATTAGTCCGAAATGCTTATGAGGCTCTCAAAAATTTAAACGAGAT 432
Db 121 AAAGACTTTATATTAGTCCGAAATGCTTATGAGGCTCTCAAAAATTTAAACGAGAT 180
OY 433 GATCATGTAGATGTTTGGATTTATTTATTTCTTATTCACACCGGTGAGTACATC 492
Db 181 GATCATGTAGATGTTTGGATTTATTTATTTCTTATTCACACCGGTGAGTACATC 240
OY 493 TATGAGAGAAATAGCCCTGCTCAAAATATTAAGTAATCATAAATTTTGGAAATCTA 552
Db 241 TATGAGAGAAATAGCCCTGCTCAAAATATTAAGTAATCATAAATTTTGGAAATCTA 300
OY 553 TTTATTTGGGAGAAATCTCAACAGAACTTAATAAGATTATTTTGAAGAAGATATC 612
Db 301 TTTATTTGGGAGAAATCTCAACAGAACTTAATAAGATTATTTTGAAGAAGATATC 360
OY 613 GTAACTTCCAGAAATGACTTTTAAATCAGAAAATCCTTATGGAATTAATTAAT 672
Db 361 GTAACTTCCAGAAATGACTTTTAAATCAGAAAATCCTTATGGAATTAATTAAT 420
OY 673 TATGACGCTACTCTCTTATGTAAGCGGAGAAATCGAAATTTGGCAC 719
Db 421 TATGACGCTACTCTCTTATGTAAGCGGAGAAATCGAAATTTGGCAC 467

```

RESULT 10
 AF055701 467 bp DNA linear BCT 22-AUG-2000
 LOCUS AF055701
 DEFINITION Streptococcus pyogenes exotoxin C (spec) gene, specs allele.

partial cds.
 ACCESSION AF055701
 VERSION AF055701.1 GI:4206383
 KEYWORDS
 SOURCE Streptococcus pyogenes
 ORGANISM Streptococcus pyogenes
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.

REFERENCE
 AUTHORS Bessen, D.E., Izzo, M.W., Florentino, T.R., Carling, R.M., Hollingshead, S.K. and Beall, B.
 TITLE Genetic linkage of exotoxin alleles and emm gene markers for tissue tropism in group A streptococci
 J. Infect. Dis. 179 (3), 627-636 (1999)
 JOURNAL 99137798
 PUBMED 9952369
 REFERENCE 2 (bases 1 to 467)
 AUTHORS Bessen, D.E., Izzo, M.W., Florentino, T.R., Carling, R.M., Hollingshead, S.K. and Beall, B.
 TITLE Direct Submission
 JOURNAL Submitted (27-MAR-1998) Epidemiology & Public Health, Yale University School of Medicine, 333 Cedar Street, Box 208034, New Haven, CT 06520, USA

FEATURES
 source Location/Qualifiers
 1. 467
 /organism="Streptococcus pyogenes"
 /mol_type="genomic DNA"
 /strain="10RS101"
 /db_xref="taxon:1314"
 <1..>467
 /gene="spec"
 /allele="spec5"
 <1..>467
 /gene="spec"
 /codon_start=1
 /transl_table=11
 /product="exotoxin C"
 /protein_id="AADI1627.1"
 /db_xref="GI:4206384"
 /translation="SNVKSLLVATTPYDKNCRVNFTHTLNDTQYRKDY
 ISSEMSYASOKFRKRDHVDVFGFLYILNSHTGTYIGTIPADNNKYNHKLGLFI
 SGESEOONNNKILIEKDIIVTFOEIDFKIRKYLMDNRYKIYDATSPYVSGRIEIGT"

gene
 CDS

BASE COUNT 177 a 70 c 70 g 150 t

ORIGIN

Query Match 49.4%; Score 462.2; DB 1; Length 467;
 Best Local Similarity 99.4%; Pred. No. 1.2e-65;
 Matches 464; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

OY 253 TCGAATGTTAAAGATTTACTTATGCAATACATACTCCTTATGATTATAAGAT 312
Db 1 TCGAATGTTAAAGATTTACTTATGCAATACATACTCCTTATGATTATAAGAT 60
OY 313 TGCAGGGTAAATTTTTCACAGCACACACATTAAACATTGATTCACAAAATATAGAGG 372
Db 61 TGCAGGGTAAATTTTTCACAGCACACACATTAAACATTGATTCACAAAATATAGAGG 120
OY 373 AAAGACTTTATATTAGTCCGAAATGCTTATGAGGCTCTCAAAAATTTAAACGAGAT 432
Db 121 AAAGACTTTATATTAGTCCGAAATGCTTATGAGGCTCTCAAAAATTTAAACGAGAT 180
OY 433 GATCATGTAGATGTTTGGATTTATTTATTTCTTATTCACACCGGTGAGTACATC 492
Db 181 GATCATGTAGATGTTTGGATTTATTTATTTCTTATTCACACCGGTGAGTACATC 240
OY 493 TATGAGAGAAATAGCCCTGCTCAAAATATTAAGTAATCATAAATTTTGGAAATCTA 552
Db 241 TATGAGAGAAATAGCCCTGCTCAAAATATTAAGTAATCATAAATTTTGGAAATCTA 300
OY 553 TTTATTTGGGAGAAATCTCAACAGAACTTAATAAGATTATTTGGAAGAATATC 612
Db 301 TTTATTTGGGAGAAATCTCAACAGAACTTAATAAGATTATTTGGAAGAATATC 360

```

QY	613	GTACCTTCGCGAAATTTGACTTTAAATGCGAAATACCTTATGATTAATTAATAAT	672
Db	361	GTACTTTCCAGCAAAATTTGACTTTAAATATCGAAATTAACCTTATGATTAATTAATAAT	420
QY	673	TATGAGCGTACTTCTCCTTATGTATGAGCGGCGCAATTCGAATTTGGCAC	719
Db	421	TATGAGCGTACTTCTCCTTATGTATGAGCGGCGCAATTCGAATTTGGCAC	467
RESULT 11			
AF321000		699 bp	DNA linear BCT 23-FEB-2001
LOCUS	AF321000		
DEFINITION	streptococcus pyogenes streptococcal pyrogenic exotoxin J (speJ)		
ACCESSION	AF321000		
VERSION	AF321000.1	GI:12584162	
KEYWORDS			
SOURCE			
ORGANISM	Streptococcus pyogenes		
REFERENCE	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
AUTHORS	Streptococcus.		
TITLE	1 (bases 1 to 699)		
JOURNAL	McCormick, J. K., Pragman, A. A., Stolpa, J. C., Leung, D. Y. and		
MEDLINE	Schlievert, P. M.		
PUBMED	Functional characterization of streptococcal pyrogenic exotoxin J,		
REFERENCE	a novel superantigen		
AUTHORS	Infect. Immun. 69 (3), 1381-1388 (2001)		
TITLE	2 (bases 1 to 699)		
JOURNAL	McCormick, J. K., Pragman, A. A., Stolpa, J. C., Leung, D. Y. and		
MEDLINE	Schlievert, P. M.		
PUBMED	Direct Submission		
REFERENCE	Submitted (12-NOV-2000) Microbiology, University of Minnesota,		
AUTHORS	Delaware St. SE, Minneapolis, MN 55455, USA		
FEATURES			
SOURCE	1..699		
LOCATION/Qualifiers			
gene	/organism="Streptococcus pyogenes"		
CDS	/mol_type="genomic DNA"		
	/db_xref="taxon:1314"		
	1..699		
	/gene="speJ"		
	1..699		
	/gene="speJ"		
	/note="SPE J; superantigen, T-cell mitogen"		
	/codon_start=1		
	/transl_table=1		
	/product="streptococcal pyrogenic exotoxin J"		
	/protein_id="AAG59819.1"		
	/db_xref="GI:12584165"		
	/translation="MKRIKILIIIVIIIFHGYSKSDSENIKDKLOLNAVAYEIIIP		
	DYKNCNIDYLTTHDFYIDISYSKKRKNSSVDESVSYITTKFKKQKVIIFGLPYFTFT		
	YDYVYIGGATPSVNSSENSKIVGNLLIDGVOOKTLINPIKIDKPIPTIOEPDKRIH		
	OYIMOTKIKYDNPNSPIYIKGLEIAINNGKHSEFNLIDATSSSTSNDIFKTKDKNTIN		
	MKDSHEDIYIMTK"		
BASE COUNT	290 a	88 c	96 g 225 t
ORIGIN			
Query Match	21.4%	Score	200.4; DB 1; Length 699;
Best Local Similarity	58.6%	Pred.	No. 3.5e-23;
Matches	367; Conservative	0; Mismatches	236; Indels 3; Gaps
QY	240	TAAAGAAGACATTTGCAATGTTAAAGATTTACTTATGCTATGACATATTAACCTCTTA	299
Db	72	TAGTGAAGAAATTTTAAAGACGTTAAGCTATCAATTAATACGATACGAATCATATCCAGT	131
QY	300	TGATTTATTAAGATTCGACGGTTAAATTTTTCGAACGACACACATTAATAACATTTGATCTCA	359
Db	132	AGATTATTCGATTTGTATATATGATTTACTTGACTACTCATCATGATTTTATATGATATTTTC	191
QY	360	AAATTTATGAGGAGAAAGCATTTATATATAGTTCGAATATGCTTATGAGGCGCTCCCAAA	419
Db	192	CAGTTATTAAGAAATTTTTCAGTTGATTCGAGTTCGAGACGCTATATTAACAACAAA	251

QY	420	ATTTTAAACGACATGATCTATCTAGAGATGGTTTTGGATTTATTTATTTCTTATTTCTTATCTGCACAC	479
QY	420	ATTTTAAACGACATGATCTATCTAGAGATGGTTTTGGATTTATTTATTTCTTATTTCTTATCTGCACAC	479
Db	252	GTTTACGAAAATACAAAAGTAATATATTTTGGTCTCCGTACATTTTACTCGTTATGA	311
QY	480	CGGTGAGTACATCTATGAGGAAATTTACGCCCTGCTCAAAA--TAAATAAGTAATTCATTA	536
Db	312	TGTTTATATATATATATATGTTGGGGTTTACACCATCATGTAACAGTAAATCGGAAATATGTA	371
QY	537	ATTATTTGGGAATCTATTTATTTTGGGGAATTCACACGAGACTTAATAACAGATTTAT	596
Db	372	AATGTACGTATTTACTAATAATAGATGGAGTCCAGCAAAAACACTAATAATATCCCATAAA	431
QY	597	TCTGAAAAGGATATTCGTAACCTTCCAGGAATATGACTTTAAATCAGAAAATACCTTAT	656
Db	432	AATGATATACCTATTTTACGATTTCAAGATTTGACTTCAAAATCAGACATATCTTAT	491
QY	657	GGATTAATTTATTAATTTATGACGCTACTTTCCTTATGTAAGCGGCAGAAATCGAAATTTG	716
Db	492	GCAAAACATACAAATTTTATGATTCCTAATTTCCCATACATTAAGAGGCAATTTAGAAATTC	551
QY	717	CACAAAGATGGGAACATGAGCAATATGACTTATTTGACTACACCAATGAAGGACTAG	776
Db	552	GATCATATGCAATTAACATGAAAGTTTAACTTATATGATCAACCTCATCTAGTACAAAG	611
QY	777	ATTCATATTTTTCGAAAATTAATAAGATAATAGATTTCAATTAATGAAGAATTTAGTCA	836
Db	612	GAGTGATATTTTTTAAAAATATTAAGCAATTAAGACTTAATATTAAGAAAGTTTCAGCCA	671
QY	837	TTTCGATATTTATCTTTGAAAATATAT	862
Db	672	TTTTCATATTTTACCTTTGGACTAAT	697
RESULT 12			
AF438523		699 bp DNA linear BCT 14-NOV-2001	
LOCUS		Streptococcus pyogenes exotoxin J precursor (speJ) gene, complete	
DEFINITION		cds.	
ACCESSION	AF438523		
VERSION	AF438523.1	GI:16923745	
KEYWORDS			
SOURCE			
ORGANISM			
		Streptococcus pyogenes	
		Streptococcus pyogenes	
		Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	
		Streptococcus.	
REFERENCE			
AUTHORS		1 (bases 1 to 699)	
TITLE		Proft,T., Moffatt,S.L., Berkahn,C.J. and Fraser,J.D.	
		Identification and characterization of novel superantigens from	
		Streptococcus pyogenes	
JOURNAL		J. Exp. Med. 189 (1), 89-102 (1999)	
MEDLINE		96093428	
PUBMED		9874566	
REFERENCE			
AUTHORS		2 (bases 1 to 699)	
TITLE		Proft,T., Arcus,V.L., Handley,V., Baker,E.N. and Fraser,J.D.	
		Immunological and biochemical characterization of streptococcal	
		pyrogenic exotoxins I and J (SPE-I and SPE-J) from Streptococcus	
		pyogenes	
JOURNAL		J. Immunol. 166 (11), 6711-6719 (2001)	
MEDLINE		21259899	
PUBMED		11359827	
REFERENCE			
AUTHORS		3 (bases 1 to 699)	
TITLE		Proft,T., Moffatt,S.L., Handley,V. and Fraser,J.D.	
JOURNAL		Direct Submission	
		Submitted (19-OCT-2001) Molecular Medicine, University of Auckland,	
		Park Rd., Auckland, New Zealand	
FEATURES			
SOURCE		1..699	
		/organism="Streptococcus pyogenes"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:1314"	
		1..699	
gene		/gene="speJ"	

CDS	1. 699	/gene="speJ"	/note="superantigen; T cell mitogen; SPE-J"	
		/codon_start=1	/transl_table=1	
		/product="exotoxin J precursor"	/protein_id="AAJ31570.1"	
		/db_xref="GI:16923746"		
BASE COUNT	290 a	88 c	96 g	225 t
ORIGIN	81g_peptide			
	/gene="speJ"			
Query Match	21.4%	Score 200.4;	DB 1;	Length 699;
Best Local Similarity	58.6%	Pred. No. 3.5e-23;		
Matches 367;	Conservative 0;	Mismatches 256;	Indels 3;	Gaps 1;
Db	240	TAAGAAGACATTTCCGATGTTAAAGTATTACTTATGACATTAACCTATTAACCTCTTA	239	
	72	TAGTGAATAATTTAAACACGCTTAAGCTACATTAATTAATGACATGCAATATACACAGT	131	
QY	300	TGATTTAAAGATTCGCGGTTAAATTTTTCACAGACACACATTAACCTGATCTCA	359	
Db	132	AGATTATACAAATTTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG	191	
QY	360	AAATATAGGGAAGACATTAATTAATTAATGATTAATGATTAATGATTAATGATTAATG	419	
Db	192	CAGTTATTAATAAATAATTTTTCAGTTGATGATGATGATGATGATGATGATGATGATG	251	
QY	420	ATTTAAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	479	
Db	252	GTTTACGAAATTAACAAAGTAAATTTTGGTCTCCGTACATTAATTTACTGTTATGA	311	
QY	480	CGGTGATCATTCTATGAGAAATTCAGGCTGCTCAAA---TTAAAGTAATGATTA	536	
Db	312	TGTTTATTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	371	
QY	537	ATTATGGAATTTCTTTATTTTCGGGAGATCTCAACGAACTTAATTAACAGATTAT	596	
Db	372	AATTGATGATTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG	431	
QY	597	TCTAGAAAAGATTCGTAACCTTCAGGAATTCGCTTAATAACAGAAATTAACCTTAT	656	
Db	432	AATGATTAACCTATTTTACATTCAGAAATTTGATCTCAAAATGACGCAATTAACCTTAT	491	
QY	657	GGATTAATTAATTAATTAATGACGTAATTCCTTATGTAAGCGGACGAATTCGAATGG	716	
Db	492	GCAAAACATTAATTAATTAATGATCCTTAATTCCTCAATCAATTAAGGCAATTAGAATTC	551	
QY	717	CACAAAGATGGAACATGAGCAATAGACTATTTATTCACCAAAATGAAGGACTAG	776	
Db	552	GATCAATGCAATTAACATGAAGTTTAACCTTAATATATCAACCTCATCTAGTACAAG	611	
QY	777	ATCAGATATTTTGGCAAAATTAAGATTAATGATTAATGATTAATGATTAATGATTAATG	836	
Db	612	GAGTATATTTTAAAAATATTAAGACATTAAGACTTAATTAATGAAAGATTTCAGCCA	671	
QY	837	TTTGATATTTATCTTGAAAAATAT 862		
Db	672	TTTGTATATTTTACCTTGACTAAT 697		
RESULT 13	AE006504	10107 bp	DNA	linear
LOCUS	AE006504/c			BCT 01-JUN-2001
DEFINITION	Streptococcus pyogenes M1 GAS strain SF370, section 33 of 167 of the complete genome.			
ACCESSION	AE006504 AE004092			

VERSION	AE006504.1	GI:13621661
KEYWORDS	Streptococcus pyogenes M1 GAS	
SOURCE	Streptococcus pyogenes M1 GAS	
ORGANISM	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.	
REFERENCE	1 (bases 1 to 10107)	
AUTHORS	Ferretti, J.J., McShan, W.M., Adji, D., Savic, D., Savic, G., Lyon, K., Primeaux, C., Szate, S.S., Surorov, A.N., Kenton, S., Lai, H., Lin, S., Qian, Y., Jia, H.G., Najjar, F.Z., Ren, Q., Zhu, H., Song, L., White, J., Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.	
TITLE	Complete genome sequence of an M1 strain of Streptococcus pyogenes	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)	
MEDLINE	21192684	
PUBMED	11296296	
REFERENCE	2 (bases 1 to 10107)	
AUTHORS	Ferretti, J.J., McShan, W.M., Adji, D., Savic, D., Savic, G., Lyon, K., Primeaux, C., Szate, S.S., Surorov, A.N., Kenton, S., Lai, H., Lin, S., Qian, Y., Jia, H.G., Najjar, F.Z., Ren, Q., Zhu, H., Song, L., White, J., Yuan, X., Clifton, S.W., Roe, B.A. and McLaughlin, R.E.	
TITLE	Direct Submission	
JOURNAL	Submitted (10-APR-2001) Department of Microbiology and Immunology, University of Oklahoma Health Sciences Center, 940 SL Young Blvd, Oklahoma City, OK 73104, USA	
FEATURES	Location/Qualifiers	
source	1. 10107	
	/organism="Streptococcus pyogenes M1 GAS"	
	/mol_type="genomic DNA"	
	/strain="SF370"	
	/serotype="M1"	
	/db_xref="taxon:160490"	
gene	complement(128..880)	
CDS	/gene="SPY0428"	
	complement(128..880)	
	/gene="SPY0428"	
	/note="Best Blastp hit = sp P15879 ARC3_CBDP MONO-ADP-RIBOSYLTRANSFERASE C3 PRECURSOR (EXOENZYME C3) >g11625586 P1 A28912 NAD+ asparagine ADP-ribosyltransferase (EC 2.4.2.-) C3 precursor - Clostridium botulinum phage (strain CST) >g11296787 emb CA41167.1 (X59039) exoenzyme C3 (Clostridium botulinum C phage) >g11505281 emb CA41768.1 (X59040) exoenzyme C3 [Clostridium botulinum D phage]"	
	/codon_start=1	
	/transl_table=1	
	/product="conserved hypothetical protein"	
	/protein_id="AAK33450.1"	
	/db_xref="GI:13621662"	
	/translation="MLKRYQIAVLILLCFSLIMQTEGLVELFVCEHYERAVGEGTP AYTFSDQKGAETLILKRWGGLYIPRAEQAAMAAYTCQAGPIWTSIDKAKGELSOL TPELRDQAOADDAATHRLVPMNIVVYVYETELRDQAGPIWTSIDKAKGELSOL LCKIRLGRYTRKHFMSSTALKNAMTRPVEYRVCVKKAKAFVPEYSAVPEVEL LFPKGCLEEVGAVYSQDQKHLHEAFKSL"	
gene	1321..1875	
	/gene="SPY0430"	
CDS	1321..1875	
	/gene="SPY0430"	
	/note="Best Blastp hit = gb AAD29424.1 AF136451.1 (AF136451) fibronectin-binding protein SFS [Streptococcus equi]"	
	/codon_start=1	
	/transl_table=1	
	/product="hypothetical protein"	
	/protein_id="AAK33451.1"	
	/db_xref="GI:13621663"	
	/translation="MLKSGFMKTRSKRFLNATLALGTTLLMAHPQAEVYSKD YMTRFGLDEDSANVPSNLKARYKGLGEGYKGLGDDIPRRRTQVPEVQPSDH GYRDYGESEGEGRKDRDLFEADDSQGGKRG	

[illegible]

[illegible]

REFERENCE AUTHORS	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus. 1 Nakagawa, I., Kurokawa, K., Yamashita, A., Nakata, M., Tomiyasu, Y., Okahashi, N., Kawabata, S., Yamazaki, K., Shida, T., Yasunaga, T., Hayashi, H., Hattori, M. and Hamada, S.
TITLE	Genome Sequence of an M3 Strain of Streptococcus pyogenes Reveals a Large-Scale Genomic Rearrangement in Invasive Strains and New Insights into Phage Evolution
JOURNAL	Genome Res. 13 (6), 1042-1055 (2003)
MEDLINE	22683278
REFERENCE AUTHORS	2 (bases 1 to 311600) Yamashita, A., Nakagawa, I., Kurokawa, K., Nakata, M., Tomiyasu, Y., Yamazaki, K., Okahashi, N., Kawabata, S., Yasunaga, T., Hattori, M., Hayashi, H. and Hamada, S.
TITLE	Direct Submission
JOURNAL	Submitted (01-MAY-2002) Ken Kurokawa, Osaka University, Genome Information Research Center: 3-1, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail: ken@gen-info.osaka-u.ac.jp, URL: http://www.gen-info.osaka-u.ac.jp/, Tel: 81-6-6879-8365, Fax: 81-6-6879-2047)
COMMENT	genome project This clone was isolated from a patient presenting with toxic shock like syndrome.
FEATURES source	Location/Qualifiers 1..311600 /organism="Streptococcus pyogenes SSI-1" /mol_type="genomic DNA" /strain="SSI-1" /db_xref="taxon:193567" 232..1587 /gene="Sps0001" 232..1587 /gene="Sps0001" /note="similar to GB:AA71535.1 (AF255728) percent identity 100 in 451 aa" /codon_start=1 /evidence=not_experimental /transl_table=11 /product="chromosomal initiator protein" /protein_id="BAC63096.1" /db_xref="GI:28810158" 1742..2878 /gene="Sps0002" 1742..2878 /note="similar to GB:AL96838.1 (AE009953) percent identity 99 in 378 aa" /codon_start=1 /evidence=not_experimental /transl_table=11 /product="putative DNA polymerase III beta subunit" /protein_id="BAC63097.1" /db_xref="GI:28810159"
gene	1742..2878 /gene="Sps0002"
CDS	1742..2878 /gene="Sps0002" /note="similar to GB:AL96838.1 (AE009953) percent identity 99 in 378 aa" /codon_start=1 /evidence=not_experimental /transl_table=11 /product="putative DNA polymerase III beta subunit" /protein_id="BAC63097.1" /db_xref="GI:28810159"
gene	2953..3150 /gene="Sps0003"
CDS	2953..3150 /gene="Sps0003"
gene	3480..4595 /gene="Sps0004"
CDS	3480..4595 /gene="Sps0004"
gene	4665..5234 /gene="Sps0005"
CDS	4665..5234 /gene="Sps0005"
gene	5237..8740 /gene="Sps0006"
CDS	5237..8740 /gene="Sps0006"
gene	8740..9140 /gene="Sps0007"
CDS	8740..9140 /gene="Sps0007"
gene	9140..9540 /gene="Sps0008"
CDS	9140..9540 /gene="Sps0008"
gene	9540..9940 /gene="Sps0009"
CDS	9540..9940 /gene="Sps0009"
gene	9940..10340 /gene="Sps0010"
CDS	9940..10340 /gene="Sps0010"
gene	10340..10740 /gene="Sps0011"
CDS	10340..10740 /gene="Sps0011"
gene	10740..11140 /gene="Sps0012"
CDS	10740..11140 /gene="Sps0012"
gene	11140..11540 /gene="Sps0013"
CDS	11140..11540 /gene="Sps0013"
gene	11540..11940 /gene="Sps0014"
CDS	11540..11940 /gene="Sps0014"
gene	11940..12340 /gene="Sps0015"
CDS	11940..12340 /gene="Sps0015"
gene	12340..12740 /gene="Sps0016"
CDS	12340..12740 /gene="Sps0016"
gene	12740..13140 /gene="Sps0017"
CDS	12740..13140 /gene="Sps0017"
gene	13140..13540 /gene="Sps0018"
CDS	13140..13540 /gene="Sps0018"
gene	13540..13940 /gene="Sps0019"
CDS	13540..13940 /gene="Sps0019"
gene	13940..14340 /gene="Sps0020"
CDS	13940..14340 /gene="Sps0020"
gene	14340..14740 /gene="Sps0021"
CDS	14340..14740 /gene="Sps0021"
gene	14740..15140 /gene="Sps0022"
CDS	14740..15140 /gene="Sps0022"
gene	15140..15540 /gene="Sps0023"
CDS	15140..15540 /gene="Sps0023"
gene	15540..15940 /gene="Sps0024"
CDS	15540..15940 /gene="Sps0024"
gene	15940..16340 /gene="Sps0025"
CDS	15940..16340 /gene="Sps0025"
gene	16340..16740 /gene="Sps0026"
CDS	16340..16740 /gene="Sps0026"
gene	16740..17140 /gene="Sps0027"
CDS	16740..17140 /gene="Sps0027"
gene	17140..17540 /gene="Sps0028"
CDS	17140..17540 /gene="Sps0028"
gene	17540..17940 /gene="Sps0029"
CDS	17540..17940 /gene="Sps0029"
gene	17940..18340 /gene="Sps0030"
CDS	17940..18340 /gene="Sps0030"
gene	18340..18740 /gene="Sps0031"
CDS	18340..18740 /gene="Sps0031"
gene	18740..19140 /gene="Sps0032"
CDS	18740..19140 /gene="Sps0032"
gene	19140..19540 /gene="Sps0033"
CDS	19140..19540 /gene="Sps0033"
gene	19540..19940 /gene="Sps0034"
CDS	19540..19940 /gene="Sps0034"
gene	19940..20340 /gene="Sps0035"
CDS	19940..20340 /gene="Sps0035"
gene	20340..20740 /gene="Sps0036"
CDS	20340..20740 /gene="Sps0036"
gene	20740..21140 /gene="Sps0037"
CDS	20740..21140 /gene="Sps0037"
gene	21140..21540 /gene="Sps0038"
CDS	21140..21540 /gene="Sps0038"
gene	21540..21940 /gene="Sps0039"
CDS	21540..21940 /gene="Sps0039"
gene	21940..22340 /gene="Sps0040"
CDS	21940..22340 /gene="Sps0040"
gene	22340..22740 /gene="Sps0041"
CDS	22340..22740 /gene="Sps0041"
gene	22740..23140 /gene="Sps0042"
CDS	22740..23140 /gene="Sps0042"
gene	23140..23540 /gene="Sps0043"
CDS	23140..23540 /gene="Sps0043"
gene	23540..23940 /gene="Sps0044"
CDS	23540..23940 /gene="Sps0044"
gene	23940..24340 /gene="Sps0045"
CDS	23940..24340 /gene="Sps0045"
gene	24340..24740 /gene="Sps0046"
CDS	24340..24740 /gene="Sps0046"
gene	24740..25140 /gene="Sps0047"
CDS	24740..25140 /gene="Sps0047"
gene	25140..25540 /gene="Sps0048"
CDS	25140..25540 /gene="Sps0048"
gene	25540..25940 /gene="Sps0049"
CDS	25540..25940 /gene="Sps0049"
gene	25940..26340 /gene="Sps0050"
CDS	25940..26340 /gene="Sps0050"
gene	26340..26740 /gene="Sps0051"
CDS	26340..26740 /gene="Sps0051"
gene	26740..27140 /gene="Sps0052"
CDS	26740..27140 /gene="Sps0052"
gene	27140..27540 /gene="Sps0053"
CDS	27140..27540 /gene="Sps0053"
gene	27540..27940 /gene="Sps0054"
CDS	27540..27940 /gene="Sps0054"
gene	27940..28340 /gene="Sps0055"
CDS	27940..28340 /gene="Sps0055"
gene	28340..28740 /gene="Sps0056"
CDS	28340..28740 /gene="Sps0056"
gene	28740..29140 /gene="Sps0057"
CDS	28740..29140 /gene="Sps0057"
gene	29140..29540 /gene="Sps0058"
CDS	29140..29540 /gene="Sps0058"
gene	29540..29940 /gene="Sps0059"
CDS	29540..29940 /gene="Sps0059"
gene	29940..30340 /gene="Sps0060"
CDS	29940..30340 /gene="Sps0060"
gene	30340..30740 /gene="Sps0061"
CDS	30340..30740 /gene="Sps0061"
gene	30740..31140 /gene="Sps0062"
CDS	30740..31140 /gene="Sps0062"
gene	31140..31540 /gene="Sps0063"
CDS	31140..31540 /gene="Sps0063"
gene	31540..31940 /gene="Sps0064"
CDS	31540..31940 /gene="Sps0064"
gene	31940..32340 /gene="Sps0065"
CDS	31940..32340 /gene="Sps0065"
gene	32340..32740 /gene="Sps0066"
CDS	32340..32740 /gene="Sps0066"
gene	32740..33140 /gene="Sps0067"
CDS	32740..33140 /gene="Sps0067"
gene	33140..33540 /gene="Sps0068"
CDS	33140..33540 /gene="Sps0068"
gene	33540..33940 /gene="Sps0069"
CDS	33540..33940 /gene="Sps0069"
gene	33940..34340 /gene="Sps0070"
CDS	33940..34340 /gene="Sps0070"
gene	34340..34740 /gene="Sps0071"
CDS	34340..34740 /gene="Sps0071"
gene	34740..35140 /gene="Sps0072"
CDS	34740..35140 /gene="Sps0072"
gene	35140..35540 /gene="Sps0073"
CDS	35140..35540 /gene="Sps0073"
gene	35540..35940 /gene="Sps0074"
CDS	35540..35940 /gene="Sps0074"
gene	35940..36340 /gene="Sps0075"
CDS	35940..36340 /gene="Sps0075"
gene	36340..36740 /gene="Sps0076"
CDS	36340..36740 /gene="Sps0076"
gene	36740..37140 /gene="Sps0077"
CDS	36740..37140 /gene="Sps0077"
gene	37140..37540 /gene="Sps0078"
CDS	37140..37540 /gene="Sps0078"
gene	37540..37940 /gene="Sps0079"
CDS	37540..37940 /gene="Sps0079"
gene	37940..38340 /gene="Sps0080"
CDS	37940..38340 /gene="Sps0080"
gene	38340..38740 /gene="Sps0081"
CDS	38340..38740 /gene="Sps0081"
gene	38740..39140 /gene="Sps0082"
CDS	38740..39140 /gene="Sps0082"
gene	39140..39540 /gene="Sps0083"
CDS	39140..39540 /gene="Sps0083"
gene	39540..39940 /gene="Sps0084"
CDS	39540..39940 /gene="Sps0084"
gene	39940..40340 /gene="Sps0085"
CDS	39940..40340 /gene="Sps0085"
gene	40340..40740 /gene="Sps0086"
CDS	40340..40740 /gene="Sps0086"
gene	40740..41140 /gene="Sps0087"
CDS	40740..41140 /gene="Sps0087"
gene	41140..41540 /gene="Sps0088"
CDS	41140..41540 /gene="Sps0088"
gene	41540..41940 /gene="Sps0089"
CDS	41540..41940 /gene="Sps0089"
gene	41940..42340 /gene="Sps0090"
CDS	41940..42340 /gene="Sps0090"
gene	42340..42740 /gene="Sps0091"
CDS	42340..42740 /gene="Sps0091"
gene	42740..43140 /gene="Sps0092"
CDS	42740..43140 /gene="Sps0092"
gene	43140..43540 /gene="Sps0093"
CDS	43140..43540 /gene="Sps0093"
gene	43540..43940 /gene="Sps0094"
CDS	43540..43940 /gene="Sps0094"
gene	43940..44340 /gene="Sps0095"
CDS	43940..44340 /gene="Sps0095"
gene	44340..44740 /gene="Sps0096"
CDS	44340..44740 /gene="Sps0096"
gene	44740..45140 /gene="Sps0097"
CDS	44740..45140 /gene="Sps0097"
gene	45140..45540 /gene="Sps0098"
CDS	45140..45540 /gene="Sps0098"
gene	45540..45940 /gene="Sps0099"
CDS	45540..45940 /gene="Sps0099"
gene	45940..46340 /gene="Sps0100"
CDS	45940..46340 /gene="Sps0100"
gene	46340..46740 /gene="Sps0101"
CDS	46340..46740 /gene="Sps0101"
gene	46740..47140 /gene="Sps0102"
CDS	46740..47140 /gene="Sps0102"
gene	47140..47540 /gene="Sps0103"
CDS	47140..47540 /gene="Sps0103"
gene	47540..47940 /gene="Sps0104"
CDS	47540..47940 /gene="Sps0104"
gene	47940..48340 /gene="Sps0105"
CDS	47940..48340 /gene="Sps0105"
gene	48340..48740 /gene="Sps0106"
CDS	48340..48740 /gene="Sps0106"
gene	48740..49140 /gene="Sps0107"
CDS	48740..49140 /gene="Sps0107"
gene	49140..49540 /gene="Sps0108"
CDS	49140..49540 /gene="Sps0108"
gene	49540..49940 /gene="Sps0109"
CDS	49540..49940 /gene="Sps0109"
gene	49940..50340 /gene="Sps0110"
CDS	49940..50340 /gene="Sps0110"
gene	50340..50740 /gene="Sps0111"
CDS	50340..50740 /gene="Sps0111"
gene	50740..51140 /gene="Sps0112"
CDS	50740..51140 /gene="Sps0112"
gene	51140..51540 /gene="Sps0113"
CDS	51140..51540 /gene="Sps0113"
gene	51540..51940 /gene="Sps0114"
CDS	51540..51940 /gene="Sps0114"
gene	51940..52340 /gene="Sps0115"
CDS	51940..52340 /gene="Sps0115"
gene	52340..52740 /gene="Sps0116"
CDS	52340..52740 /gene="Sps0116"
gene	52740..53140 /gene="Sps0117"
CDS	52740..53140 /gene="Sps0117"
gene	53140..53540 /gene="Sps0118"
CDS	53140..53540 /gene="Sps0118"
gene	53540..53940 /gene="Sps0119"
CDS	53540..53940 /gene="Sps0119"
gene	53940..54340 /gene="Sps0120"
CDS	53940..54340 /gene="Sps0120"
gene	54340..54740 /gene="Sps0121"
CDS	54340..54740 /gene="Sps0121"
gene	54740..55140 /gene="Sps0122"
CDS	54740..55140 /gene="Sps0122"
gene	55140..55540 /gene="Sps0123"
CDS	55140..55540 /gene="Sps0123"
gene	55540..55940 /gene="Sps0124"
CDS	55540..55940 /gene="Sps0124"
gene	55940..56340 /gene="Sps0125"
CDS	55940..56340 /gene="Sps0125"
gene	56340..56740 /gene="Sps0126"
CDS	56340..56740 /gene="Sps0126"
gene	56740..57140 /gene="Sps0127"
CDS	56740..57140 /gene="Sps0127"
gene	57140..57540 /gene="Sps0128"
CDS	57140..57540 /gene="Sps0128"
gene	57540..57940 /gene="Sps0129"
CDS	57540..57940 /gene="Sps0129"
gene	57940..58340 /gene="Sps0130"
CDS	57940..58340 /gene="Sps0130"
gene	58340..58740 /gene="Sps0131"
CDS	58340..58740 /gene="Sps0131"
gene	58740..59140 /gene="Sps0132"
CDS	58740..59140 /gene="Sps0132"
gene	59140..59540 /gene="Sps0133"
CDS	59140..59540 /gene="Sps0133"
gene	59540..59940 /gene="Sps0134"
CDS	59540..59940 /gene="Sps0134"
gene	59940..60340 /gene="Sps0135"
CDS	59940..60340 /gene="Sps0135"
gene	60340..60740 /gene="Sps0136"
CDS	60340..60740 /gene="Sps0136"
gene	60740..61140 /gene="Sps0137"
CDS	60740..61140 /gene="Sps0137"
gene	61140..61540 /gene="Sps0138"
CDS	61140..61540 /gene="Sps0138"
gene	61540..61940 /gene="Sps0139"
CDS	61540..61940 /gene="Sps0139"
gene	61940..62340 /gene="Sps0140"
CDS	61940..62340 /gene="Sps0140"
gene	62340..62740 /gene="Sps0141"
CDS	62340..62740 /gene="Sps0141"
gene	62740..63140 /gene="Sps0142"
CDS	62740..63140 /gene="Sps0142"
gene	63140..63540 /gene="Sps0143"
CDS	63140..63540 /gene="Sps0143"
gene	63540..63940 /gene="Sps0144"
CDS	63540..63940 /gene="Sps0144"
gene	63940..64340 /gene="Sps0145"
CDS	63940..6434

THIS PAGE BLANK (USPTO)